



Db	241	CCCAAGCTCTCGAGCGAGCGCCCTGAGCCCGCGGTCGCCGAGACCGCGTGAAGCTCTCGAGGCGCAT	300
QY	301	GGAGCGCGCGCTCCCGTCAACGGGCGCGCTGAACGCTTCGGGGGGCGCTGGCGGGCGATCGCGC	360
Db	301	GGAGCGCGCGCGCGCCCGACGGGCGCGCTAAACGCTTCGGGGGGCGCTGGCGGGCGATGCGCGC	360
QY	361	GGCGGCGGGGCGGGGGCGCGCGCTTCGCGGACGCGCTGAACCGCGGGGCTGGCGCGCGCAT	420
Db	361	GGCGGCGGGGCGGGGGCGCGCGCTTCGCGGACGCGCTGAACCGCGGGGCTGGCGCGCGCAT	420
QY	421	GGCGCGTGCATCTGTAAGCACGGTGTCTGGGCAACGGCGTGTGATCATGTCCGCTTCGTGGC	480
Db	421	GGCGCGTGCATCTGTAAGCACGGTGTCTGGGCAACGGCGTGTGATCATGTCCGCTTCGTGGC	480
QY	481	CGACTCGAGGCTCCGCAACCCAGAAACAATTCTTCCTGCTCAACTCCGCATCTCCGACTT	540
Db	481	CGACTCGAGGCTCCGCAACCCAGAAACAATTCTTCCTGCTCAACTCCGCATCTCCGACTT	540
QY	541	CCTGTGAGGCGCTTCGTGCATCCCACTGTATGTACCTAAGGTGACGAGCGCGTGGAC	600
Db	541	CCTGTGAGGCGCTTCGTGCATCCCACTGTATGTACCTAAGGTGACGAGCGCGTGGAC	600
QY	601	CTTCGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGTGACTAAGCTGTGCAACTCTCTC	660
Db	601	CTTCGGCGGGGCGCTCTGCAAGCTGTGGCTGGTAGTGACTAAGCTGTGCAACTCTCTC	660
QY	661	TGCGTTCACAATCGTGTCTATCAGTACGACCGCGTTCCTGTGGGTACCCGAGCGGTCTC	720
Db	661	TGCGTTCACAATCGTGTCTATCAGTACGACCGCGTTCCTGTGGGTACCCGAGCGGTCTC	720
QY	721	ATACCGGGGCGGACGAGGGGTGAACGCGGGCGGGCAGTGGGAAAGATGCTGGTGTGGGT	780
Db	721	ATACCGGGGCGGACGAGGGGTGAACGCGGGCGGGCAGTGGGAAAGATGCTGGTGTGGGT	780
QY	781	GCTGGCTCTTCGTCGTATGAGACGACGCACTCTGAGCTGGGAGTACCTGTCCGGGGCGAG	840
Db	781	GCTGGCTCTTCGTCGTATGAGACGACGCACTCTGAGCTGGGAGTACCTGTCCGGGGCGAG	840
QY	841	CTGCATCCCGGAGGGGCACTGTGTATGCGGAGTCTTCTTCAACACTGTGATCTTCATCAC	900
Db	841	CTGCATCCCGGAGGGGCACTGTGTATGCGGAGTCTTCTTCAACACTGTGATCTTCATCAC	900
QY	901	GGCTTCACCCCTGGAGTCTTTTAAGCCCTTCCTCAAGCGTCAACCTTCTTAACTTCAGAT	960
Db	901	GGCTTCACCCCTGGAGTCTTTTAAGCCCTTCCTCAAGCGTCAACCTTCTTAACTTCAGAT	960
QY	961	CTACCTGAACATCCAGAGGAGCGACCCGCGCTCCGAGTGTGGGTCTGAGAGGACGCGG	1020
Db	961	CTACCTGAACATCCAGAGGAGCGACCCGCGCTCCGAGTGTGGGTCTGAGAGGACGCGG	1020
QY	1021	CCCGAGGCTCCCTCCGAGGCCCGAGCGCTCAACACCCCGACCGCGCTGGCTGTGGGGGTG	1080
Db	1021	CCCGAGGCTCCCTCCGAGGCCCGAGCGCTCAACACCCCGACCGCGCTGGCTGTGGGGGTG	1080
QY	1081	CTGGGAGAAAGGGGACCGGGAGGCGCATCCGCTGACAGTATGGGGTGGGTGTAGGCGGC	1140
Db	1081	CTGGGAGAAAGGGGACCGGGAGGCGCATCCGCTGACAGTATGGGGTGGGTGTAGGCGGC	1140
QY	1141	CGTAGGCGCTGTAGGCGCGGGAGAGCGACCTCCGAGGGGTGGCGGTGGGAGCGGCTCCGTGGC	1200
Db	1141	CGTAGGCGCTGTAGGCGCGGGAGAGCGACCTCCGAGGGGTGGCGGTGGGAGCGGCTCCGTGGC	1200
QY	1201	TTCAACCACTTCAGACTCCGGAGCTCTCTGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
Db	1201	TTCAACCACTTCAGACTCCGGAGCTCTCTGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
QY	1261	GAGGGGCTTCAGAGCGGTGGCGTCTCTCGGCGCTCGCTGGAAGAGCGCATGAAGATGTGTCT	1320
Db	1261	GAGGGGCTTCAGAGCGGTGGCGTCTCTCGGCGCTCGCTGGAAGAGCGCATGAAGATGTGTCT	1320
QY	1321	CCAGAGCTTCACCCAGCGGCTTTCGGCTGTCTCTGGGACAGAAAGTGGCGCAAGTGGCTGGC	1380
Db	1321	CCAGAGCTTCACCCAGCGGCTTTCGGCTGTCTCTGGGACAGAAAGTGGCGCAAGTGGCTGGC	1380

QY	1381	GTGATGTAAGCATCTTTGGGAGCTGTGTGGGGCCCAATACAGCTGTGATGATCATCCG	1440
DB	1381	CGTATGATGAGCATCTTTGGGAGCTGTGTGGGGCCCAATACAGCTGTGATGATCATCCG	1440
QY	1441	GAGCGCTGTGCATGAGGCCACATCCGTCCCTGACTACTGTGTAGAAACCTCTCTTGGCTCT	1500
DB	1441	GAGCGCGTGCATGAGGCCACATCCGTCCCTGACTACTGTGTAGAAACCTCTCTTGGCTCT	1500
QY	1501	GTGGGCCAATCTGGGCTGTCAACCTGTCTCTTACCTCTGTGGCAACAAGCTTCGGCCG	1560
DB	1501	GTGGGCCAATCTGGGCTGTCAACCTGTCTCTTACCTCTGTGGCAACAAGCTTCGGCCG	1560
QY	1561	GGCGTTACCAAGGTGCTGTGGCCCCCGAAGAGCTCAAAATCAGAGCCCAAGCTCCCTGGA	1620
DB	1561	GGCGTTACCAAGGTGCTGTGGCCCCCGAAGAGCTCAAAATCAGAGCCCAAGCTCCCTGGA	1620
QY	1621	GCATGTGTGAAATGAGTGTGGCCCAAGAGCTTCCTCTCAGCCACAGCTCTTCTAGCCCAAG	1680
DB	1621	GCATGTGTGAAATGAGTGTGGCCCAAGAGCTTCCTCTCAGCCACAGCTCTTCTAGCCCAAG	1680
QY	1681	GTCCTCTGGGCAATGTGGAGCTGTGGCCCTGACCCCTGACCCGAGCTGATCCCGCAGGGGTGAGCC	1740
DB	1681	GTCCTCTGGGCAATGTGGAGCTGTGGCCCTGACCCCTGACCCGAGCTGATCCCGCAGGGGTGAGCC	1740
QY	1741	CGCGGTGTCTGTGGCCCTCTCTTTAATGCAAGCAAGCAACCTCTCCATGTGAGAGGCGCTTC	1800
DB	1741	CGCGGTGTCTGTGGCCCTCTCTTTAATGCAAGCAAGCAACCTCTCCATGTGAGAGGCGCTTC	1800
QY	1801	CTGGGTTTGGCCAGAGGGGCCCTCACTGAGCTGGAATGTGAGGCTGGGTGGAGCGCCCTGACC	1860
DB	1801	CTGGGTTTGGCCAGAGGGGCCCTCACTGAGCTGGAATGTGAGGCTGGGTGGAGCGCCCTGACC	1860
QY	1861	CCCAATTCTTGGCTCAACCGGGGAGGAGCAAGTCTGAAGGTCCAGACATCTGTGCCACCC	1920
DB	1861	CCCAATTCTTGGCTCAACCGGGGAGGAGCAAGTCTGAAGGTCCAGACATCTGTGCCACCC	1920
QY	1921	CCTGTGTGTGCCACCTTGTGGCAAGTACTGTGTGTGTCTTCCCAAGCAAGCAACTGTG	1980
DB	1921	CCTGTGTGTGCCACCTTGTGGCAAGTACTGTGTGTGTCTTCCCAAGCAAGCAACTGTG	1980
QY	1981	GTGTGCTCTCAAGGCTTCTCGGCCCTGTAGAGTTTGCTCTGTGACAGTGCACACACTTGCACACC	2040
DB	1981	GTGTGCTCTCAAGGCTTCTCGGCCCTGTAGAGTTTGCTCTGTGACAGTGCACACACTTGCACACC	2040
QY	2041	CCTGCACACACTTGCACACCGTCTCTCCCGGACAAAGCCAGGACATGTGCTTGTCTG	2100
DB	2041	CCTGCACACACTTGCACACCGTCTCTCCCGGACAAAGCCAGGACATGTGCTTGTCTG	2100
QY	2101	CGTTCTGTCTCTTGCATTAAGCTCTAAGGCTGTGGCCCTTTTCAACCTCTTTCCACCAACTCT	2160
DB	2101	CGTTCTGTCTCTTGCATTAAGCTCTAAGGCTGTGGCCCTTTTCAACCTCTTTCCACCAACTCT	2160
QY	2161	CTGTGGCCCCCAAAAGTGTCAAGGGGCCCTGTAGAACTGTGAAGCTGTCTGTGCTTTTCA	2220
DB	2161	CTGTGGCCCCCAAAAGTGTCAAGGGGCCCTGTAGAACTGTGAAGCTGTCTGTGCTTTTCA	2220
QY	2221	TTCTGGGTGTCTTTCAGAAAGTGTGAAGAAACATCTCTGTGAACCTTGAATGTTCGTGGG	2280
DB	2221	TTCTGGGTGTCTTTCAGAAAGTGTGAAGAAACATCTCTGTGAACCTTGAATGTTCGTGGG	2280
QY	2281	ATGTGTTAATCAAGAGAGCAAAATTTGTGTGAGAGCTCAGGGCTGTGATTTGGCAGAGTGTGGG	2340
DB	2281	ATGTGTTAATCAAGAGAGCAAAATTTGTGTGAGAGCTCAGGGCTGTGATTTGGCAGAGTGTGGG	2340
QY	2341	CTCCCAAGCCCTCTCTCCCTCGCTTAAAGCTTTCGGGCTGAGTGTGTGCAAGCTGTCTTGTGCC	2400
DB	2341	CTCCCAAGCCCTCTCTCCCTCGCTTAAAGCTTTCGGGCTGAGTGTGTGCAAGCTGTCTTGTGCC	2400
QY	2401	CACCCCGCTCTGGGCTCAACAACAGCCCTGTGGCCAAAGCCGTGCCCGGAGCAACTGTGTTT	2460
DB	2401	CACCCCGCTCTGGGCTCAACAACAGCCCTGTGGCCAAAGCCGTGCCCGGAGCAACTGTGTTT	2460

QY 2461 GCTCACCCAGACCTCTGGGGGTTGTTGGAGAGAGGGGCCCGGCTGGCCCGAGGGGTC 2520  
|  
|  
|  
DB 2461 GCTCACCCAGACCTCTGGGGGTTGTTGGAGAGAGGGGCCCGGCTGGCCCGAGGGGTC 2520  
|  
|  
|  
QY 2521 CAAGGCGTGCAGGGGCGGTCCAGAGAGAGGTGCCCGGGCAGGGGCGCTTCGACATGTGCT 2580  
|  
|  
|  
DB 2521 CAAGGCGTGCAGGGGCGGTCCAGAGAGAGGTGCCCGGGCAGGGGCGCTTCGACATGTGCT 2580  
|  
|  
|  
QY 2581 GTGGACCCCGTGCAGGGGCGGTTCGATGCTCCCTGCTGTGCCCCGCTGGCCCTGCA 2640  
|  
|  
|  
DB 2581 GTGGACCCCGTGCAGGGGCGGTTCGATGCTCCCTGCTGTGCCCCGCTGGCCCTGCA 2640  
|  
|  
|  
QY 2641 AACCGTAGGTCAACATAAAGTATTTTAAAAA 2699  
|  
|  
|  
DB 2641 AACCGTAGGTCAACATAAAGTATTTTAAAAA 2699  
|  
|  
|  
RESULT 2  
BD235872 2699 bp DNA linear PART 17-JUL-2003  
LOCUS Isolated DNA encoding human H3 histamine receptor.  
DEFINITION BD235872  
ACCESSION BD235872.1 GI:33045642  
VERSION JP 2002526049-A/5.  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM  
other sequences; artificial sequences.  
1 (bases 1 to 2699)  
Labenberg, T.W., Erlander, M., Huber, A. and Piatel, J.  
Isolated DNA encoding human H3 histamine receptor  
Patent: JP 2002526049-A 5 20-AUG-2002;  
ORTHO MCNEIL PHARMACEUTICAL INC  
COMMENT  
OS Artificial Sequence  
PN JP 2002526049-A/5  
PD 20-AUG-2002  
PF 07-OCT-1998 JP 2000573370  
PI /TIMOTHY W LABENBERG, MARK ERLANDER, ARNE HUBER, JIYAVASYURY PI  
PIATEL  
PC C12N15/09, A61K38/00, A61K45/00, A61P3/04, A61P3/10, A61P9/06, PC  
A61P25/16,  
PC A61P25/18, A61P25/22, A61P25/24, A61P25/28, C07K14/705, C07K16/28,  
PC C12N1/15,  
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/02, C12Q1/68 PC  
, G01N33/15, G01N33/50,  
PC C12N15/00, A61K37/02, C12N5/00  
CC Description of Artificial Sequence: CDNA  
FH Key Location/Qualifiers  
FT source 1..2699  
Location/Qualifiers  
1..2699  
1.2699  
/organism="Artificial Sequence".  
FEATURES  
Source  
1..2699  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN  
Query Match 100.0%; Score 2699; DB 6; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CAACGCTCCGCGGTGACCGGTGCACCGGACGGGCTCAGGCTCCGGCTCTCTCC 60  
|  
|  
|  
DB 1 CAACGCTCCGCGGTGACCGGTGCACCGGACGGGCTCAGGCTCCGGCTCTCTCC 60  
|  
|  
|  
QY 61 GTTGACAGACCGCGGTGCGGGCCCACTGGGCTCCGGCCCGGCTCCCTGCA 120  
|  
|  
|  
DB 61 GTTGACAGACCGCGGTGCGGGCCCACTGGGCTCCGGCCCGGCTCCCTGCA 120  
|  
|  
|  
QY 121 CGGCTGCTCTGGGCGCGGGCCCGGCGGCGGACCATGCTGGGCGCCCCCAAGGAGAA 180  
|  
|  
|  
DB 121 CGGCTGCTCTGGGCGCGGGCCCGGCGGCGGACCATGCTGGGCGCCCCCAAGGAGAA 180  
|  
|  
|  
QY 181 ACCGACCCGCGCAAGGGCCCGCAAGAGAGAGGCTCCGGGCGGGGCCCTCCCGGCGG 240  
|  
|  
|

DB 181 ACCGACCCGCGCAAGGGCCCGCAAGAGAGGCTCCGGGCGGGGCCCTCCCGGCGG 240  
|  
|  
|  
QY 241 CCCAGCTCTGGGCGGGCGGCTCCCGGCTCCCGAGCGCGGTAGCCTGGGGGCGCAT 300  
|  
|  
|  
DB 241 CCCAGCTCTGGGCGGGCGGCTCCCGGCTCCCGAGCGGGGTAGCCTGGGGGCGCAT 300  
|  
|  
|  
QY 301 GGAGGCGCGCGCGCGCAAGGGCGGCTGAACGCTTCGGGGGCGCTGGCGGGGCAATGCGGC 360  
|  
|  
|  
DB 301 GGAGGCGCGCGCGCGCGCAAGGGCGGCTGAACGCTTCGGGGGCGCTGGCGGGGCAATGCGGC 360  
|  
|  
|  
QY 361 GGGGCGGGCGGGGCGCGCGGCTTCGAGCAGCTTGAACCGGCGGTGGCGCGCTCAT 420  
|  
|  
|  
DB 361 GGGGCGGGCGGGGCGCGCGGCTTCGAGCAGCTTGAACCGGCGGTGGCGCGCTCAT 420  
|  
|  
|  
QY 421 GGGCGTCTCATCTGTGGCCAGCGGTGCTGGGCAACGCGCTGTGATGCTGCTGTGGC 480  
|  
|  
|  
DB 421 GGGCGTCTCATCTGTGGCCAGCGGTGCTGGGCAACGCGCTGTGATGCTGCTGTGGC 480  
|  
|  
|  
QY 481 CGACTCGAGCCCTCCGACCCGACCAACACTTCTCGGTGCTCAACCTGGCCATCCGACTT 540  
|  
|  
|  
DB 481 CGACTCGAGCCCTCCGACCCGACCAACACTTCTCGGTGCTCAACCTGGCCATCCGACTT 540  
|  
|  
|  
QY 541 CCTCGTGGCGGCTTCGTCATCCACTGTATGTAACCTGATGTCAGACGCGCTGAC 600  
|  
|  
|  
DB 541 CCTCGTGGCGGCTTCGTCATCCACTGTATGTAACCTGATGTCAGACGCGCTGAC 600  
|  
|  
|  
QY 601 CTTGCGCGGGGCGCTTCGCAAGCTGTGCTGTGATGTAACCTGCTGTGCACTCTTC 660  
|  
|  
|  
DB 601 CTTGCGCGGGGCGCTTCGCAAGCTGTGCTGTGATGTAACCTGCTGTGCACTCTTC 660  
|  
|  
|  
QY 661 TGGCTTCAACATCTGTGCTCATAGCTAACAACGCTTCCTGTGGGTACCGGCGGCTTC 720  
|  
|  
|  
DB 661 TGGCTTCAACATCTGTGCTCATAGCTAACAACGCTTCCTGTGGGTACCGGCGGCTTC 720  
|  
|  
|  
QY 721 ATACGGGGCCGACAGAGGTGACACCGGCGGCGAGTGCAGAAAGATGCTGATGAGT 780  
|  
|  
|  
DB 721 ATACGGGGCCGACAGAGGTGACACCGGCGGCGAGTGCAGAAAGATGCTGATGAGT 780  
|  
|  
|  
QY 781 GCTGGCTTCTGCTGTGACGACACAGCCATCTGAGCTGGAGTACCTTCGCGGGGCGAG 840  
|  
|  
|  
DB 781 GCTGGCTTCTGCTGTGACGACACAGCCATCTGAGCTGGAGTACCTTCGCGGGGCGAG 840  
|  
|  
|  
QY 841 CTCATCCCGGAGGCGCACTGTATGCGAGTCTTCAACAATGCTATCTCTCAATCAC 900  
|  
|  
|  
DB 841 CTCATCCCGGAGGCGCACTGTATGCGAGTCTTCAACAATGCTATCTCTCAATCAC 900  
|  
|  
|  
QY 901 GGGCTTCAACCTGGAGTCTTACGCGCTTCCTCAGACGTCACCTTCTTAACCTCAGCAT 960  
|  
|  
|  
DB 901 GGGCTTCAACCTGGAGTCTTACGCGCTTCCTCAGACGTCACCTTCTTAACCTCAGCAT 960  
|  
|  
|  
QY 961 CTACTGAACATCTCAGAGGCGGACCGGCTTCGGCTGTAGTGGGCTCGAGAGGACGCGG 1020  
|  
|  
|  
DB 961 CTACTGAACATCTCAGAGGCGGACCGGCTTCGGCTGTAGTGGGCTCGAGAGGACGCGG 1020  
|  
|  
|  
QY 1021 CCGCGAGCCCTCCCGAGGCGGACCGGCTTCGGCTGTAGTGGGCTCGAGAGGACGCGG 1080  
|  
|  
|  
DB 1021 CCGCGAGCCCTCCCGAGGCGGACCGGCTTCGGCTGTAGTGGGCTCGAGAGGACGCGG 1080  
|  
|  
|  
QY 1081 CTGGAGAAAGGGGCAAGGGGAGGAGGCTGACAGGTATGGGGTGGGTGAGGCGGCG 1140  
|  
|  
|  
DB 1081 CTGGAGAAAGGGGCAAGGGGAGGAGGCTGACAGGTATGGGGTGGGTGAGGCGGCG 1140  
|  
|  
|  
QY 1141 CGTAGGCGCTGAGGCGGAGGAGGAGCCCTTCGAGGAGTGGGCTGGGCGGCTCGTGGC 1200  
|  
|  
|  
DB 1141 CGTAGGCGCTGAGGCGGAGGAGGAGCCCTTCGAGGAGTGGGCTGGGCGGCTCGTGGC 1200  
|  
|  
|  
QY 1201 TTCAACCACTTCAAGTCTGGGAGGCTCTTCAGAGGGGCACTAGAGAGGCGCGCTCACTCAA 1260  
|  
|  
|  
DB 1201 TTCAACCACTTCAAGTCTGGGAGGCTCTTCAGAGGGGCACTAGAGAGGCGCGCTCACTCAA 1260  
|  
|  
|  
QY 1261 GAGGGGCTCAAGCGGTGCGGCTTCCTGGGCTCGCTGAGAGAGCGCATGAAGATGATGTC 1320  
|  
|  
|

Db 1261 GAGGGGCTCCAAAGCCGTCGCTCTCGGCTCGCTGAGAAAGCATGAGATGATGTC 1320  
Qy 1321 CCAGAGCTTACCCAGAGCTTTCGGCTGCTCGGAGCAGAGAAAGTGGCCAGTGGTGGC 1380  
Db 1321 CCAGAGCTTACCCAGAGCTTTCGGCTGCTCGGAGCAGAGAAAGTGGCCAGTGGTGGC 1380  
Qy 1381 GGTATGCTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATGATCAG 1440  
Db 1381 GGTATGCTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATGATCAG 1440  
Qy 1441 GGGGGGCTGAGCAGTGGCTGCTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1500  
Db 1441 GGGGGGCTGAGCAGTGGCTGCTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1500  
Qy 1501 GTGGGCACTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1560  
Db 1501 GTGGGCACTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1560  
Qy 1561 GGGCTTTCACCAAGCTGCTGCTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1620  
Db 1561 GGGCTTTCACCAAGCTGCTGCTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1620  
Qy 1621 GAGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1680  
Db 1621 GAGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1680  
Qy 1681 GTCTCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1740  
Db 1681 GTCTCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1740  
Qy 1741 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1800  
Db 1741 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1800  
Qy 1801 GTGGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1860  
Db 1801 GTGGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1860  
Qy 1861 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1920  
Db 1861 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1920  
Qy 1921 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1980  
Db 1921 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 1980  
Qy 1981 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2040  
Db 1981 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2040  
Qy 2041 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2100  
Db 2041 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2100  
Qy 2101 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2160  
Db 2101 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2160  
Qy 2161 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2220  
Db 2161 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2220  
Qy 2221 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2280  
Db 2221 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2280  
Qy 2281 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2340  
Db 2281 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2340  
Qy 2341 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2400  
Db 2341 GGGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2400

Qy 2401 CACCCGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2460  
Db 2401 CACCCGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2460  
Qy 2461 GGTATGCTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATGATCAG 2520  
Db 2461 GGTATGCTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATGATCAG 2520  
Qy 2521 GGGGGGCTGAGCAGTGGCTGCTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2580  
Db 2521 GGGGGGCTGAGCAGTGGCTGCTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2580  
Qy 2581 GTGACCCGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2640  
Db 2581 GTGACCCGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2640  
Qy 2641 AACCGTGAAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2699  
Db 2641 AACCGTGAAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 2699

RESULT 3  
AR217194 2699 bp DNA linear PAT 25-SEP-2002  
LOCUS AR217194  
DEFINITION Sequence 5 from patent US 6413743.  
ACCESSION AR217194  
VERSION AR217194.1 GI:23316634  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
1..2699  
/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN  
Query Match 100.0%; Score 2699; DB 6; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCAAGCGTCCGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 60  
Db 1 CCAAGCGTCCGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 60  
Qy 61 GGTGAGAGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 120  
Db 61 GGTGAGAGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 120  
Qy 121 CCGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 180  
Db 121 CCGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 180  
Qy 181 ACCGACCCGCGGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 240  
Db 181 ACCGACCCGCGGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 240  
Qy 241 CCGAGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 300  
Db 241 CCGAGCTGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 300  
Qy 301 GAGAGCGCGCGCGCGGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 360  
Db 301 GAGAGCGCGCGCGCGGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 360  
Qy 361 GGGGCGGCGCGCGCGGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 420  
Db 361 GGGGCGGCGCGCGCGGAGCGGCGGCTGAGTGTGAGTCCCTGATCTAGTGTGAGAAAGTCTCTTGGTCT 420







```
Db 1621 GCACTGCTGGAAGTAGTGAGCCCAACGAGGCGCTCCCTGACGCCACGCTCTCTGACGCCAG 1680
Qy 1681 GCTCTCTGAGGCACTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Db 1681 GCTCTCTGAGGCACTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740
Qy 1741 GCGCGGTGCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Db 1741 GCGCGGTGCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1800
Qy 1801 CTGGGTTGCGCAGAGGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Db 1801 CTGGGTTGCGCAGAGGAGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860
Qy 1861 CCGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Db 1861 CCGACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1920
Qy 1921 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Db 1921 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1980
Qy 1981 GGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Db 1981 GGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2040
Qy 2041 CCTGCAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Db 2041 CCTGCAACACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2100
Qy 2101 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Db 2101 CCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2160
Qy 2161 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Db 2161 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
Qy 2221 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Db 2221 TTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280
Qy 2281 ATGTTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Db 2281 ATGTTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340
Qy 2341 CTCCACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Db 2341 CTCCACGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400
Qy 2401 CACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Db 2401 CACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
Qy 2461 GCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Db 2461 GCTGACCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2520
Qy 2521 CAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Db 2521 CAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580
Qy 2581 GTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Db 2581 GTGACACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Qy 2641 AACCGTAGAGTCAATTAAGTATTTTAAAAA 2699
Db 2641 AACCGTAGAGTCAATTAAGTATTTTAAAAA 2699
```

RESULT 5

```
AF140538
LOCUS AF140538 2699 bp mRNA linear PRI 10-JUN-1999
DEFINITION Homo sapiens histamine H3 receptor mRNA, complete cds.
ACCESSION AF140538
VERSION AF140538.1 GI:5031290
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2699)
Loveberg, T.W., Roland, B.L., Wilson, S.J., Jiang, X., Pyati, J.,
Huvar, A., Jackson, M.R. and Erlender, M.E.
Cloning and functional expression of the human histamine H3
receptor.
Mol. Pharmacol. 55 (6), 1101-1107 (1999)
JOURNAL
MEDLINE 99278519
PUBMED 10347254
REFERENCE
AUTHORS 2 (bases 1 to 2699)
Loveberg, T.W., Roland, B.R., Wilson, S.J., Jiang, X., Pyati, J.,
Huvar, A., Jackson, M.R. and Erlender, M.E.
Direct Submission
Submitted (05-Apr-1999) Molecular Pharmacology, RW Johnson PRI,
3535 General Atomics Ct, San Diego, CA 92121, USA
FEATURES
source
1..2699
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
299..1636
/codon_start=1
/product="histamine H3 receptor"
/protein_id="AAD38151.1"
/db_xref="GI:5031291"
/translation="MERAAPDGPILNAGSLADGAAAGARGFSAWTLAALMAL
IVATVGNALVWLAEVADSLRTONNFFLNIAIDFLVAGACIPLVYVLTGRWTF
GRGLKLMVVDVYLCTSSAENVILVLSIDRFVTRAVSRADQDTRAVRKLMLW
VLAPLILYGPALISMEYVLSGGSSIPRGHCYAEFFMYWPLITSLTEFPPLPSLYPFG
LSTVNLIDRRLRLDGAERAEAPPEPPADQSPPPPPPCWQWQHEANPLHRYG
VGEAAVGAAGAGATVGGGGGVSAPSSSSSSSSRGERPPSLKRGSPSSASABLE
KMKMVSQSFTRFRLSRDRKVAKSLAVVLSFGLCMAPVLTLMITIRAAQCHGCVDPY
WYETSFWLIMNSAVNPVLYPLCHHSFRAPFKLLCPQLKIQPHSLBHCWK"
ORIGIN
Query Match 100.0%; Score 2699; DB 9; Length 2699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCAACGCTCCGCGGCTGCAAGCTGCAACCGGACAGGCTCAAGCTCCGCGCTCTCTCC 60
Db 1 CCAACGCTCCGCGGCTGCAAGCTGCAACCGGACAGGCTCAAGCTCCGCGCTCTCTCC 60
Qy 61 GCTGACAGACCGCGCTGCGGCGCCCACTGGGCTGGATCCGAGCCCGGCGCCCTTGCGGA 120
Db 61 GCTGACAGACCGCGCTGCGGCGCCCACTGGGCTGGATCCGAGCCCGGCGCCCTTGCGGA 120
Qy 121 CCGCTGCTCTGAGCCCGGCGCCCGGCGCCCGAGACCATGCTGGGCGGCCCGCAGGGAA 180
Db 121 CCGCTGCTCTGAGCCCGGCGCCCGGCGCCCGAGACCATGCTGGGCGGCCCGCAGGGAA 180
Qy 181 ACCCGACCCGCGCAGAGGCGCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 ACCCGACCCGCGCAGAGGCGCCGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Qy 241 CCAAGCTCTGAGCGCGGCGCTGCGCGCGTCCGAGAGCGAGTGAAGCTGAGCGGAGCGCAT 300
Db 241 CCAAGCTCTGAGCGCGGCGCTGCGCGCGTCCGAGAGCGAGTGAAGCTGAGCGGAGCGCAT 300
Qy 301 GGAAGCGCGCGCGCGCTGAGCGGCGCTGAAAGCTTTCGAGAGCGCTGAGCGAGCGATCGGC 360
Db 301 GGAAGCGCGCGCGCGCGCTGAGCGGCGCTGAAAGCTTTCGAGAGCGCTGAGCGAGCGATCGGC 360
Qy 361 GAGCGCGCGCGCGCGCGCTTCTCGGACGCTGAGACCGGCGGTGCTGCGCGCGCTCAT 420
```



QY 2581 GNGACCCGCTGCGAGCGCTGCGATGCTCTGCTGCGCGCGCTGCGCTGCGCTGCA 2640  
| | | | |  
Db 2581 GNGACCCGCTGCGAGCGCTGCGATGCTCTGCTGCGCGCGCTGCGCTGCGCTGCA 2640  
| | | | |  
QY 2641 AACCGTAGGTCACATATAAGTATTTTAAAAA 2699  
| | | | |  
Db 2641 AACCGTAGGTCACATATAAGTATTTTAAAAA 2699  
| | | | |  
RESULT 6  
ARI04201 2689 bp DNA linear PAT 14-FEB-2001  
LOCUS Sequence 1 from patent US 6093545.  
ACCESSION ARI04201  
VERSION ARI04201.1 GI:12816909  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 2689)  
AUTHORS Goodheart, A.D.J. and Glucksmann, M. Alexandra.  
TITLE Methods for detecting nucleic acid molecules encoding a member of  
the muscarinic family of receptors  
JOURNAL Patent: US 6093545-A 1 25-JUL-2000;  
FEATURES Location/Qualifiers  
source 1..2689  
/organism="unknown"  
/mol\_type="unassigned DNA"

Query Match 97.6%; Score 2635.2; DB 6; Length 2689;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 25 CGCACCGGAGCGGCTCAAGGCTCCGGCTCTCTCCGCTGCGAGACCGCGCTGCGGCGC 84  
| | | | |  
Db 18 CGCACCGGAGCGGCTCAAGGCTCCGGCTCTCTCCGCTGCGAGACCGCGCTGCGGCGC 77  
| | | | |  
QY 85 CCACCTGGGCTCGGATCCGGCCCGCGCGCGCTCGGCGACCGGCTGCTGCGCGCGCGC 144  
| | | | |  
Db 78 CCACCTGGGCTCGGATCCGGCCCGCGCGCGCTCGGCGACCGGCTGCTGCGCGCGCGC 137  
| | | | |  
QY 145 GCGCCGCGGACCATCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 204  
| | | | |  
Db 138 GCGCCGCGGACCATCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 196  
| | | | |  
QY 205 AAGACGAGGCTCCCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 264  
| | | | |  
Db 197 AAGACGAGGCTCCCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 256  
| | | | |  
QY 265 CCGCGCTCCCGGAGCGCGCTGAGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGC 324  
| | | | |  
Db 267 CCGCGCTCCCGGAGCGCGCTGAGCGCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGC 316  
| | | | |  
QY 325 GCTGAACGCTTGGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 384  
| | | | |  
Db 317 GCTGAACGCTTGGGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTT 376  
| | | | |  
QY 385 CCGGAGCGCTGAGACCGCGGCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 444  
| | | | |  
Db 377 CCGGAGCGCTGAGACCGCGGCTGCTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 436  
| | | | |  
QY 445 GCTGGGCAACCGCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 504  
| | | | |  
Db 437 GCTGGGCAACCGCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 496  
| | | | |  
QY 505 CAACCTTCTTCTGCTCAACCTGCGCATCTTCGCACTTCTGCTGCTGCTGCTGCTGCTGCT 564  
| | | | |  
Db 497 CAACCTTCTTCTGCTCAACCTGCGCATCTTCGCACTTCTGCTGCTGCTGCTGCTGCTGCT 556  
| | | | |  
QY 565 ACTGATGATACCTTACGCTGCTGAGAGCGCGCTGAGACTTCCGCGCGGCGCGCTGCAAGCT 624  
| | | | |

Db 557 ACTGATGATACCTTACGCTGCTGAGAGCGCGCTGAGACTTCCGCGCGGCGCGCTGCAAGCT 616  
| | | | |  
QY 625 GNGCGTAGAGGAGTACTGCTGCGACCTCTCTGCTTCAACATGCTGCTACAG 684  
| | | | |  
Db 617 GNGCGTAGAGGAGTACTGCTGCGACCTCTCTGCTTCAACATGCTGCTACAG 676  
| | | | |  
QY 685 CTACGACCGCTTCTGCTGCGTCAACCGAGCGGCTCTCATCTCCGCGCGCGCGCGCGAG 744  
| | | | |  
Db 677 CTACGACCGCTTCTGCTGCGTCAACCGAGCGGCTCTCATCTCCGCGCGCGCGCGAG 736  
| | | | |  
QY 745 GCGGCGGAGAGTCCGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 804  
| | | | |  
Db 737 GCGGCGGAGAGTCCGGAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 796  
| | | | |  
QY 805 AGCATCTGAGCTGAGAGTACTGCTGCGGCGCGAGCTCATCTCCGAGGCGCATCTGCTA 864  
| | | | |  
Db 797 AGCATCTGAGCTGAGAGTACTGCTGCGGCGCGAGCTCATCTCCGAGGCGCATCTGCTA 856  
| | | | |  
QY 865 TGCAGAGTCTTCTCAACTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 924  
| | | | |  
Db 857 TGCAGAGTCTTCTCAACTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 916  
| | | | |  
QY 925 GCGCTTCTCAAGCGTCACTTCTTAACTCAAGCATCTAAGCATCAAGAGCGGCGAC 984  
| | | | |  
Db 917 GCGCTTCTCAAGCGTCACTTCTTAACTCAAGCATCTAAGCATCAAGAGCGGCGAC 976  
| | | | |  
QY 985 CCGCTCCGCTGAGATGCGGCTCGAGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1044  
| | | | |  
Db 977 CCGCTCCGCTGAGATGCGGCTCGAGAGGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 1036  
| | | | |  
QY 1045 GCGCTCACACCCCGGCGCTGAGCTGCGGCGGCTGCTGCGGAGAGGCGAGGCGC 1104  
| | | | |  
Db 1037 GCGCTCACACCCCGGCGCTGAGCTGCGGCGGCTGCTGCGGAGAGGCGAGGCGC 1096  
| | | | |  
QY 1105 CATGCGGCTGCA CAGATATGAGGTGAGTGAAGCGCGCGCTGAGCGCTGAGCGCGGAGGC 1164  
| | | | |  
Db 1097 CATGCGGCTGCA CAGATATGAGGTGAGTGAAGCGCGCGCTGAGCGCTGAGCGCGGAGGC 1156  
| | | | |  
QY 1165 GACCTTCCGCGGCTGCGGCTGCGGCGGCGGCTGCGGCTTCAACCTCAAGCTCCGCGCAG 1224  
| | | | |  
Db 1157 GACCTTCCGCGGCTGCGGCTGCGGCGGCGGCTGCGGCTTCAACCTCAAGCTCCGCGCAG 1216  
| | | | |  
QY 1225 CTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTC 1284  
| | | | |  
Db 1217 CTCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTC 1276  
| | | | |  
QY 1285 CTGCGGCTTCTGAGAGAGCGGATGAGTGTGCTCCAGAGCTTCAACCGCGCTTTCG 1344  
| | | | |  
Db 1277 CTGCGGCTTCTGAGAGAGCGGATGAGTGTGCTCCAGAGCTTCAACCGCGCTTTCG 1336  
| | | | |  
QY 1345 GCTGTCTCGGAGCAGGAAAGTGGCCAGTCTGCTGCGCGCTCATCTGAGCATCTTGGGCT 1404  
| | | | |  
Db 1337 GCTGTCTCGGAGCAGGAAAGTGGCCAGTCTGCTGCGCGCTCATCTGAGCATCTTGGGCT 1396  
| | | | |  
QY 1405 CTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1464  
| | | | |  
Db 1397 CTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTG 1456  
| | | | |  
QY 1465 CCTGACTAGTGTGAGAACTCTCTTCTGAGCTCTGCTGAGGCGCAACTCGGCTGTCAACC 1524  
| | | | |  
Db 1457 CCTGACTAGTGTGAGAACTCTCTTCTGAGCTCTGCTGAGGCGCAACTCGGCTGTCAACC 1516  
| | | | |  
QY 1525 TGTCTCTTACCTCTGCTGCGACCAAGCTTCCGCGGCGGCTTCAACAGCTGCTGCTGCC 1584  
| | | | |  
Db 1517 TGTCTCTTACCTCTGCTGCGACCAAGCTTCCGCGGCGGCTTCAACAGCTGCTGCTGCC 1576  
| | | | |  
QY 1585 CCAAGAGCTCAAAATCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1644  
| | | | |  
Db 1577 CCAAGAGCTCAAAATCCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1636  
| | | | |  
QY 1645 CCAAGAGCTCTCTCAAGCGGCGGCTCTCAAGCGGCGGCTCTCTGAGCATCTGAGCTGCT 1704  
| | | | |  
Db 1637 CCAAGAGCTCTCTCAAGCGGCGGCTCTCTCAAGCGGCGGCTCTCTGAGCATCTGAGCTGCT 1696  
| | | | |

```

OY 1705 GCGCCCTACCCGCGCTGTTCCCGCAGGGGTAGCCCGCGGTGTCTGTGGCCCTCTCTTA 1764
DB 1697 GCGCCCTACCCGCGCTGTTCCCGCAGGGGTAGCCCGCGGTGTCTGTGGCCCTCTCTTA 1756
OY 1765 ATGCCACGCGACCGACCCCTGCGCATGAGAGCGCCCTTCTGTGGTTGGCCAGAGGGCCCTCTCA 1824
DB 1757 ATGCCACGCGACCGACCCCTGCGCATGAGAGCGCCCTTCTGTGGTTGGCCAGAGGGCCCTCTCA 1816
OY 1825 CTGGCTGAGCTGAGAGGCTGGGTGGCGCGCCCTGCCCCACATTTGGGTCTCCACCGCGGA 1884
DB 1817 CTGGCTGAGCTGAGAGGCTGGGTGGCGCGCCCTGCCCCACATTTGGGTCTCCACCGCGGA 1875
OY 1885 GGGAGAGTCTGGAGGTGCCAGACATGCTGCCACCCCTGCTGTGTGCCACCCCTTGCAG 1944
DB 1876 GGGAGAGTCTGGAGGTGCCAGACATGCTGCCACCCCTGCTGTGTGCCACCCCTTGCAG 1935
OY 1945 TTACTGTGTGTGTGTCTTCCCAAGACAGACCTGGGTGTCTCCAGGCTTCTTGCCTTA 2004
DB 1936 TTACTGTGTGTGTGTCTTCCCAAGACAGACCTGGGTGTCTCCAGGCTTCTTGCCTTA 1995
OY 2005 GAGTGTGTCTGACGTCGACACACCTGACACCCCTGACACACCTGACACCCCTTGC 2064
DB 1996 GAGTGTGTCTGACGTCGACACACCTGACACCCCTGACACACCTGACACCCCTTGC 2055
OY 2065 CTCTCCCGGACAGCCGACGACCTGCTGTGCTCTTCTGTCTTTCATTAAGCCTC 2124
DB 2056 CTCTCCCGGACAGCCGACGACCTGCTGTGCTCTTCTGTCTTTCATTAAGCCTC 2115
OY 2125 AGGCTGCGCCCTTTCACCCCTTTCACACACCTCTCTGTGCCCCCAAAAGTGTCAAGG 2184
DB 2116 AGGCTGCGCCCTTTCACCCCTTTCACACACCTCTCTGTGCCCCCAAAAGTGTCAAGG 2175
OY 2185 GCGCTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATTCGTGGGTGTTCAGAAAGATGA 2244
DB 2176 GCGCTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATTCGTGGGTGTTCAGAAAGATGA 2235
OY 2245 AGAAGAAAAATGTCTGTGAATGTTCTGTGGATGTTTATCAAGAGACAAAT 2304
DB 2236 AGAAGAAAAATGTCTGTGAATGTTCTGTGGATGTTTATCAAGAGACAAAT 2295
OY 2305 TGCTAGAGAGCTCAGAGGCTGAGATTGGCAGGTGTGGCTTCCACGCCCTCTCCCTCGCT 2364
DB 2296 TGCTAGAGAGCTCAGAGGCTGAGATTGGCAGGTGTGGCTTCCACGCCCTCTCCCTCGCT 2355
OY 2365 AAGGCTTCGAGCTGAGCTGTGTCAGCTGCTTCCGACCCGCGCTGTGGGTCAACCA 2424
DB 2356 AAGGCTTCGAGCTGAGCTGTGTCAGCTGCTTCCGACCCGCGCTGTGGGTCAACCA 2415
OY 2425 GCGCTGTGCGCAACCTGCTGCCGCACTGTGTTTGTCAACCGAGACCTTGTGGGGTT 2484
DB 2416 GCGCTGTGCGCAACCTGCTGCCGCACTGTGTTTGTCAACCGAGACCTTGTGGGGTT 2475
OY 2485 GTTGGGAGAGAGGGGCGCGGCTGGGCTCGAAGGCTCCCAAGGCTGTGAGGGGCTTCAGA 2544
DB 2476 GTTGGGAGAGAGGGGCGCGGCTGGGCTCGAAGGCTCCCAAGGCTGTGAGGGGCTTCAGA 2535
OY 2545 GAGAGTGCCTGGGAGGGGCGGCTTCGAGATGTGTGTCACCCGTCACAGCGCGCTGC 2604
DB 2536 GAGAGTGCCTGGGAGGGGCGGCTTCGAGATGTGTGTCACCCGTCACAGCGCGCTGC 2595
OY 2605 ATGCTCTCTGCTGTGCGCGCTGCGCTGCGCTGCAACCGTGAAGTCAATTAAGTGT 2664
DB 2596 ATGCTCTCTGCTGTGCGCGCTGCGCTGCGCTGCAACCGTGAAGTCAATTAAGTGT 2655
OY 2665 ATTTTATTAATAAAAAAAAAAAAAA 2688
DB 2656 ATTTTATTAATAAAAAAAAAAAAAA 2679

```

```

RESULT 7
BD086285          2689 bp      DNA      linear      PART 27-AUG-2002
LOCUS

```

```

DEFINITION  G protein-coupled receptor and utilization thereof.
ACCESSION  BD086285
VERSION    BD086285.1  GI:22631895
KEYWORDS   JP 2001525174-A/1.
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 (bases 1 to 2689)
AUTHORS   Goodearl,A.D.J., Glucksmann,A.M., Xie,M. and Distefano,P.
TITLE     G protein-coupled receptor and utilization thereof
JOURNAL   Patent: JP 2001525174-A 11-DEC-2001;
          MILLENNium PHARMACEUTICALS INC
COMMENT    OS Unidentified
          PN JP 2001525174-A/1
          PD 11-DEC-2001
          PE 04-DEC-1998 JP 2000523346
          PR 04-DEC-1997 US 08/985090 17-MAR-1998 US 09/042780 PT
          ANDREW D J GOODEARL, ALEXANDRA M GLUCKSMANN, MICHAEL XIE, PETER PI
          DISTEFANO
          PC C12N15/09,C07K14/705,C07K16/28,C12N5/10,C12P21/02,C12Q1/68//
          CC (C12P21/02,C12R1:91),C12N15/00,C12N5/00
          CC Strandedness: Single;
          CC Topology: linear;
          CC G protein-coupled receptor and utilization thereof FH Key
FEATURES
  source          FT      CDS
                   Location/Qualifiers
                   1..2689
                   /organism="unidentified"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:32644"
ORIGIN
Query Match          97.6%; Score 2635.2; DB 6; Length 2689;
Beet Local Similarity 99.8%; Pred. No. 0;
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;
OY 25 GCGACGCGCAGCGGCTCAGGCTCCGGCTCTCTCCGCTGACAGACGCGCTGCGGCC 84
DB 18 CGACCGCAGCGGCTCAGGCTCCGGCTCTCTCCGCTGACAGACGCGCTGCGGCC 77
OY 85 CCACCTGGGCTGGATCCGCGCCCGCCCGCCCTCTGAGACCGGCTGTGTGGCCCGCCCG 144
DB 78 CCACCTGGGCTGGATCCGCGCCCGCCCGCCCTCTGAGACCGGCTGTGTGGCCCGCCCG 137
OY 145 GCGCCGCGGACCATGCGCTGAGGCGCGCCCGCAGAGGAAACCGACCCGCGCAAGGCGCGCA 204
DB 138 GCGCCGCGGACCATGCGCTGAGGCGCGCCCGCAGAGGAAACCGACCCGCGCGCA 196
OY 205 AAGACGAGGCTCCCGGCGCGGCGCCCTCCGCGCGCCGACGCTCTGAGCGCGCTTGC 264
DB 197 AAGACGAGGCTCCCGGCGCGGCGCCCTCCGCGCGCCGACGCTCTGAGCGCGCTTGC 256
OY 265 CCGCGCTCCCGGACCGCGGTGAGCTGTGGGGCCATGAGAGCGCGCGCCCGCAAGGCGC 324
DB 257 CCGCGGTCCCGAGCGCGGTGAGCTGTGGGGCCATGAGAGCGCGCGCCCGCAAGGCGC 316
OY 325 GGTGAAGCTTCGAGGAGGCGGTGAGCGGCGATGCGGCGGCGGCGGAGCGCGGCGCTT 384
DB 317 GGTGAAGCTTCGAGGAGGCGGTGAGCGGCGATGCGGCGGCGGAGCGCGGCGCTT 376
OY 385 CTGCGACCTGAGACCGCGGTGCTGGCGCGCTCAATGAGCGCTGCTCATGTGGCCACGAT 444
DB 377 CTGCGACCTGAGACCGCGGTGCTGGCGCGCTCAATGAGCGCTGCTCATGTGGCCACGAT 436
OY 445 GCTGGGCAACCGCGCTGTGATGCTGTGCTTGTGTGCGCGCATGTGAGCTTCCGACCCAGAA 504
DB 437 GCTGGGCAACCGCGCTGTGATGCTGTGCTTGTGTGCGCGCATGTGAGCTTCCGACCCAGAA 496
OY 505 CAACCTTCTTCGCTCAACCTGACATCTCGACCTTCTCGCGGCGCTTCTGATCC 564
DB 497 CAACCTTCTTCGCTCAACCTGACATCTCGACCTTCTCGCGGCGCTTCTGATCC 556

```



565 ACTGATGATACCTTACGCTGACAGCGCTGGAACCTTCCGCGGGGCTCTGACAGCT 624  
557 ACTGATGATACCTTACGCTGACAGCGCTGGAACCTTCCGCGGGGCTCTGACAGCT 616  
625 GTGGCTGGTATGGAATACCTGCTGTGACCTCTCTGCTTCAACATGCTGCTCAACG 684  
617 GTGGCTGGTATGGAATACCTGCTGTGACCTCTCTGCTTCAACATGCTGCTCAACG 676  
685 CTACGACCGCTTCTGTGGGTGACCGGACGGCTCATACCGGGGGCCAGAGGGTGAAC 744  
677 CTACGACCGCTTCTGTGGGTGACCGGACGGCTCATACCGGGGGCCAGAGGGTGAAC 736  
745 GCGGCGGAGAGTGGGAGATGCTGTGGTGTGGTGTGCTGAGCTTCTGTGCTGATACGAC 804  
737 GCGGCGGAGAGTGGGAGATGCTGTGGTGTGGTGTGCTGAGCTTCTGTGCTGATACGAC 796  
805 AGCATCTGAGCTGGGAGTACCTGTCCGCGGGGACCTCCATCCCGAGGGCCACTGTCTA 864  
797 AGCATCTGAGCTGGGAGTACCTGTCCGCGGGGACCTCCATCCCGAGGGCCACTGTCTA 856  
865 TGGCGAGTCTTCTACAACTGGTACTTCTCATCAGGCTTCCACCTCGAGATTTCTTAC 924  
857 TGGCGAGTCTTCTACAACTGGTACTTCTCATCAGGCTTCCACCTCGAGATTTCTTAC 916  
925 GGCCTTCTCAGCGTCACTTCTTAACTCAGCATCTACCTGAACATCAGAGGCGAC 984  
917 GGCCTTCTCAGCGTCACTTCTTAACTCAGCATCTACCTGAACATCAGAGGCGAC 976  
985 GCGCTTCCGCGTGGATGGGGCTTGAAGAGCAGCGGGCCCGAGCCCTCCGAGGCCA 1044  
977 GCGCTTCCGCGTGGATGGGGCTTGAAGAGCAGCGGGCCCGAGCCCTCCGAGGCCA 1036  
1045 GGCCTTCAACACCCCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104  
1037 GGCCTTCAACACCCCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096  
1105 CATGCGCTGCAACAGTATGGGGTGGGTGAGGCGCGCTGAGGCGCTGAGGCGCGGGAGGC 1164  
1097 CATGCGCTGCAACAGTATGGGGTGGGTGAGGCGCGCTGAGGCGCTGAGGCGCGGGAGGC 1156  
1165 GACCTTCCGCGGCTGGCGGTGGGGGCGGCTCCGCTGCTTCAACCACTCCAGCTCCGCGAG 1224  
1157 GACCTTCCGCGGCTGGCGGTGGGGGCGGCTCCGCTGCTTCAACCACTCCAGCTCCGCGAG 1216  
1225 CTCTCTGAGAGGCACTGAGAGGCGCGGCTCACTCAAGAGGGGCTCCAAGCGTCCGCGTTC 1284  
1217 CTCTCTGAGAGGCACTGAGAGGCGCGGCTCACTCAAGAGGGGCTCCAAGCGTCCGCGTTC 1276  
1285 CTGCGGCTCGCTGAGAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCGAGGCTTTCG 1344  
1277 CTGCGGCTCGCTGAGAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCGAGGCTTTCG 1336  
1345 GCTGTCTCGGGAACAGAAAGTGGCCAAAGTGGCTGCGCTCATCTGAGAGCTTTGGGCT 1404  
1337 GCTGTCTCGGGAACAGAAAGTGGCCAAAGTGGCTGCGCTCATCTGAGAGCTTTGGGCT 1396  
1405 CTGCTGAGGCGCCCACTACGCTGCTGATGATCAATCCGCGCGCTGCTGCTGCTGCTGCTGCT 1464  
1397 CTGCTGAGGCGCCCACTACGCTGCTGATGATCAATCCGCGCGCTGCTGCTGCTGCTGCTGCT 1456  
1465 CCTGACTACTGAGTGAAGAACTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1524  
1457 CCTGACTACTGAGTGAAGAACTCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1516  
1525 TGTCTCTTACCTCTGTGCAACAGCTTCCGCGGGGCTTCAACCAAGCTGCTGCTGCTGCT 1584  
1517 TGTCTCTTACCTCTGTGCAACAGCTTCCGCGGGGCTTCAACCAAGCTGCTGCTGCTGCTGCT 1576  
1585 CCAAGAACTCAAAATTCAGGCCCAAGCTTCCCTGAGACCTGCTGAGAGTGAAGTGGCCCA 1644  
1577 CCAAGAACTCAAAATTCAGGCCCAAGCTTCCCTGAGACCTGCTGAGAGTGAAGTGGCCCA 1636  
1645 CCAAGAACTTCCCTGAGACCAAGCTTCTGAGGCCAGGTCTCTGGGCAATCTGGCCTGCT 1704

1637 CCAAGAACTTCCCTGAGACCAAGCTTCTGAGGCCAAGTCTCGTGGGCAATCTGGCCTGCT 1696  
1705 GGCCTTACCGGCTGCTTCCCAAGGGTGAAGCCCGCGGTGTCTGTGGCCTTCTTTA 1764  
1697 GGCCTTACCGGCTGCTTCCCAAGGGTGAAGCCCGCGGTGTCTGTGGCCTTCTTTA 1756  
1765 ATGCCAAGGAGCAACCTCGCATGAGAGGCGCTTCTGTGGGTGAGCAGAGGGCCCTCA 1824  
1757 ATGCCAAGGAGCAACCTCGCATGAGAGGCGCTTCTGTGGGTGAGCAGAGGGCCCTCA 1816  
1825 CTGGCTGACTGAGAGGCTGGGTGGCCGGCTGCGCCCGCCCAATCTGGCTTCAACCGGGA 1884  
1817 CTGGCTGACTGAGAGGCTGGGTGGCCGGCTGCGCCCGCCCAATCTGGCTTCAACCGGGA 1875  
1885 GGGACAGTCTGAGAGTCCAGACATGCTGCCAACCCCTGTGGTGGCCACCTTGGCAG 1944  
1876 GGGACAGTCTGAGAGTCCAGACATGCTGCCAACCCCTGTGGTGGCCACCTTGGCAG 1935  
1945 TTACTGGTGTGTTCTTCCAAAGCAACCTGGGTGTGCTCCAGGCTTCCGCTGCTCA 2004  
1936 TTACTGGTGTGTTCTTCCAAAGCAACCTGGGTGTGCTCCAGGCTTCCGCTGCTCA 1995  
2005 GCAATTTGCTCTGACAGTGCACACCTGACACACCTGACACACCTGACACACCTGAC 2064  
1996 GCAATTTGCTCTGACAGTGCACACCTGACACACCTGACACACCTGACACACCTGAC 2055  
2065 CTCTCCCGGAGCAAGCCAGACACTGCTCTTGTGCTGCTTGTCTTGTGATAGCTTC 2124  
2056 CTCTCCCGGAGCAAGCCAGACACTGCTCTTGTGCTGCTTGTCTTGTGATAGCTTC 2115  
2125 AGGCTGGGCTTTTCAACCCCTTCCACCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2184  
2116 AGGCTGGGCTTTTCAACCCCTTCCACCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 2175  
2185 GGCCTAGGAACCTCGAAGCTGTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2244  
2176 GGCCTAGGAACCTCGAAGCTGTTCTGCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2235  
2245 AGAAGAAACATGTCTGTGAACCTTGAATGTTCTGTGGATGTTTAAATCAGAGACAAAT 2304  
2236 AGAAGAAACATGTCTGTGAACCTTGAATGTTCTGTGGATGTTTAAATCAGAGACAAAT 2295  
2305 TGTCTAGAGGCTCAGAGGCTGATTTGGCAGGTGGGCTTCCAGGCTTCTCTCTGCTGCT 2364  
2296 TGTCTAGAGGCTCAGAGGCTGATTTGGCAGGTGGGCTTCCAGGCTTCTCTCTGCTGCT 2355  
2365 AAGGCTTCCGCGTGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2424  
2356 AAGGCTTCCGCGTGAAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2415  
2425 GGCCTGTGGCCAAAGCTGCGCCCGGCACTCTGTTTGTCTCAACCAAGACCTTGGGGGTT 2484  
2416 GGCCTGTGGCCAAAGCTGCGCCCGGCACTCTGTTTGTCTCAACCAAGACCTTGGGGGTT 2475  
2485 GTTGGAGAGAGGGGCGCGGCTGGGCTCGAGGGTCCAAAGGCTGTGCAAGGGGCTGTCAGA 2544  
2476 GTTGGAGAGAGGGGCGCGGCTGGGCTCGAGGGTCCAAAGGCTGTGCAAGGGGCTGTCAGA 2535  
2545 GGAAGGCGCCGGGAGGGGCGCTTCCGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2604  
2536 GGAAGGCGCCGGGAGGGGCGCTTCCGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2595  
2605 ATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2664  
2596 ATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2655  
2665 ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2688  
2656 ATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 2679

RESULT 8



CO730452  
LOCUS CO730452 2665 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 16386 from Patent WO02068579.  
ACCESSION CO730452  
VERSION CO730452.1 GI:42304323  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.  
Kites, such as nucleic acid arrays, comprising a majority of  
humaneons or transcripts, for detecting expression and other uses  
hereof  
JOURNAL Patent: WO 02068579-A 16386 06-SEP-2002;  
PE Corporation (US)  
FEATURES  
Source  
1..2665  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
ORIGIN  
Query Match 97.5%; Score 2632; DB 6; Length 2665;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2657; Conservative 0; Mismatches 5; Indels 2; Gaps 2;  
QY 10 CCGCGGCTGCAAGGTGGACCGGCAAGGCTCAAGGTCGGGCTCTCTCCCTCCGCTGACAGA 69  
DB 4 CTCGGCTGACAGTGTGACCGGCAAGGCTCAAGGTCGGGCTCTCTCCCTCCGCTGACAGA 63  
QY 70 GCGGCGCTGCGGCGCCCACTGGGCTGAGATCCGCGCCCGGCGCCCTCGGCAAGCGCTGCT 129  
DB 64 GCGGCGCTGCGGCGCCCACTGGGCTGAGATCCGCGCCCGGCGCCCTCGGCAAGCGCTGCT 123  
QY 130 CTGGGCGCGGCGCGCGCGCGCGGACATGCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCG 189  
DB 124 CTGGGCGCGGCGCGCGCGCGCGGACATGCGCTGGGCGCGCGCGCGCGCGCGCGCGCGCG 182  
QY 190 GCGGCAAGGCGCGGCAAGGCGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 249  
DB 183 GCGGCAAGGCGCGGCAAGGCGGCTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 242  
QY 250 GCGGCGGCGCGCTGCGCGCGCGCGCGGAGCGCGGAGCGCTGCGGCGCGCGCGCGCGCGCG 309  
DB 243 GCGGCGGCGCGCTGCGCGCGCGCGCGGAGCGCGGAGCGCTGCGGCGCGCGCGCGCGCGCG 302  
QY 310 GCGGCGGCGCGCGCTGCGCGCGCGCGCGGAGCGCGGAGCGCTGCGGCGCGCGCGCGCGCG 369  
DB 303 GCGGCGGCGCGCGCTGCGCGCGCGCGCGGAGCGCGGAGCGCTGCGGCGCGCGCGCGCGCG 362  
QY 370 GCGGCGGCGCGCGCTGCGCGCGCGCGCGGAGCGCGGAGCGCTGCGGCGCGCGCGCGCGCG 429  
DB 363 GCGGCGGCGCGCGCTGCGCGCGCGCGCGGAGCGCGGAGCGCTGCGGCGCGCGCGCGCGCG 422  
QY 430 CATGCGGCGCGAGTGGGCAAGCGCGTGGTCAATGCTGCGCTTGTGAGCGCGAGCTGAG 489  
DB 423 CATGCGGCGCGAGTGGGCAAGCGCGTGGTCAATGCTGCGCTTGTGAGCGCGAGCTGAG 482  
QY 490 CCGCGGCGCGAGCAACACTTCTTCTGTGCAACCTGCGCAATCTCGGACTCTCTGCTGCG 549  
DB 483 CCGCGGCGCGAGCAACACTTCTTCTGTGCAACCTGCGCAATCTCGGACTCTCTGCTGCG 542  
QY 550 CCGCTTGTGCAATCCCACTGATATGATACCTTACGCTGCTGAGACAGGCGGCTGAGACCTT 609  
DB 543 CCGCTTGTGCAATCCCACTGATATGATACCTTACGCTGCTGAGACAGGCGGCTGAGACCTT 602  
QY 610 GCGGCGCTGCAAGCTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 669  
DB 603 GCGGCGCTGCAAGCTGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 662  
QY 670 CATGCTGCTCATGAGTACGACCGCTTCTGTGTGCTACCGGAGGCTCTCATACCGGAGC 729

DB 663 CATGCTGCTCATGAGTACGACCGCTTCTGTGTGCTACCGGAGGCTCTCATACCGGAGC 722  
QY 730 CCAGCAGGAGTGCACAGCGCGCGGCGAGTGGGAAAGTGTGCTGATGGGCTGAGGCTT 789  
DB 723 CCAGCAGGAGTGCACAGCGCGCGGCGAGTGGGAAAGTGTGCTGATGGGCTGAGGCTT 782  
QY 790 CCGTGTGTAACGAGCAGGCAATCTGAGCTGGGAGTACTGTGTCGGGAGGCAAGCTTCATCC 849  
DB 783 CCGTGTGTAACGAGCAGGCAATCTGAGCTGGGAGTACTGTGTCGGGAGGCAAGCTTCATCC 842  
QY 850 CGAGGCGCACTGCTATGCGGAGTCTTCTTACAACTGTAATCTTCTTCACTACGAGCTTCCAC 909  
DB 843 CGAGGCGCACTGCTATGCGGAGTCTTCTTACAACTGTAATCTTCTTCACTACGAGCTTCCAC 902  
QY 910 CCGGAGTCTCTTATGAGCTTCTCTGAGGCTCACTTCTTAACTCCAGATCTACCTGAA 969  
DB 903 CCGGAGTCTCTTATGAGCTTCTCTGAGGCTCACTTCTTAACTCCAGATCTACCTGAA 962  
QY 970 CATCCAGAGGCGCACCGGCTTCCGCTGAGATGGGCTCGAGAGGCGAGCGCGCGAGCC 1029  
DB 963 CATCCAGAGGCGCACCGGCTTCCGCTGAGATGGGCTCGAGAGGCGAGCGCGCGAGCC 1022  
QY 1030 CCTCTCCGAGGCGCACCGGCTTCCGCTGAGATGGGCTCGAGAGGCGAGCGCGCGAGCC 1089  
DB 1023 CCTCTCCGAGGCGCACCGGCTTCCGCTGAGATGGGCTCGAGAGGCGAGCGCGCGAGCC 1082  
QY 1090 GCGGCGAGGAGGCGCATGCGGCTGACAGAGTATGGGAGGAGTGGGCGCGGCTGAGGCGC 1149  
DB 1083 GCGGCGAGGAGGCGCATGCGGCTGACAGAGTATGGGAGGAGTGGGCGCGGCTGAGGCGC 1142  
QY 1150 TGAGGCGGAGGAGGCGACCTTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1209  
DB 1143 TGAGGCGGAGGAGGCGACCTTGGGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1202  
QY 1210 CTCGAGCTTCCGCACTCTCTGAGGAGGCACTGAGAGGCGCGGCTCACTCAAGAGGCGCTC 1269  
DB 1203 CTCGAGCTTCCGCACTCTCTGAGGAGGCACTGAGAGGCGCGGCTCACTCAAGAGGCGCTC 1262  
QY 1270 CAAGCGTGGGCGTCTGCGGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1329  
DB 1263 CAAGCGTGGGCGTCTGCGGCTGCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1322  
QY 1330 CACCCAGGCGCTTTCGCGCTGCTCGGAGCAGGAAAGTGGCCAAAGTGGCCGCTCATCGT 1389  
DB 1323 CACCCAGGCGCTTTCGCGCTGCTCGGAGCAGGAAAGTGGCCAAAGTGGCCGCTCATCGT 1382  
QY 1390 GAGCATCTTTGGGCTGTGCTGGGCGCCATACAGCTGCTGATGATCATTCGGGCGGCTGT 1449  
DB 1383 GAGCATCTTTGGGCTGTGCTGGGCGCCATACAGCTGCTGATGATCATTCGGGCGGCTGT 1442  
QY 1450 CCATGAGCACTGCGGCTGCTGAGTACTGAGTACGAAACCTCTTCTGAGCTCTGAGGAGC 1509  
DB 1443 CCATGAGCACTGCGGCTGCTGAGTACTGAGTACGAAACCTCTTCTGAGCTCTGAGGAGC 1502  
QY 1510 CTGCGCTGTCAACCTGTCTCTTCACTCTGTGCAACCAAGCTTCCGCGGAGCTTCAAC 1569  
DB 1503 CTGCGCTGTCAACCTGTCTCTTCACTCTGTGCAACCAAGCTTCCGCGGAGCTTCAAC 1562  
QY 1570 CAAGCTGCTTGCCTCCCGAGAGCTCAAAATCCAGGCGCCACAGCTTCTTGAAGACTGCTG 1629  
DB 1563 CAAGCTGCTTGCCTCCCGAGAGCTCAAAATCCAGGCGCCACAGCTTCTTGAAGACTGCTG 1622  
QY 1630 GAAAGTGAAGGCGCCACAGAGCTGCTGAGCAGGCGCTGAGGCGGAGGCTGAGGCGGCTG 1689  
DB 1623 GAAAGTGAAGGCGCCACAGAGCTGCTGAGCAGGCGCTGAGGCGGAGGCTGAGGCGGCTG 1682  
QY 1690 GCATGTGAGGCGCTGAGGCGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1749  
DB 1683 GCATGTGAGGCGCTGAGGCGGCTTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1742  
QY 1750 TGTGCGCTTCTTATATGCAAGGAGCGACCTGCAATGAGAGGCGCTTCTGAGGCTTGG 1809

```

Db      1743 TGTGGCCCTCTCTTAATGCGACGGCAGCCACCTGCGCATGAGGCGCTTCTCGGTTGG 1802
Qy      1810 CCAGAGGGCCCTCATATGGCTGGAATGAGAGCTGGGTGGCCGGCCCTTGCCCCCAATATC 1869
Db      1803 CCAGAGGGCCCTCATATGGCTGGAATGAGAGCTGGGTGGCCGGCCCTTGCCCCCAATATC 1862
Qy      1870 TGGCTTCACCGGAGGAGCAAGCTGAGAGTCCAGACATGCTGAGCCACCCCTGCTGGT 1929
Db      1863 TGGCTTCACCGGAGGAGCAAGCTGAGAGTCCAGACATGCTGAGCCACCCCTGCTGGT 1921
Qy      1930 GCCACACCTTTCGAGTACTGTTGTTGTTCTTCCAAAGACAGCACTGGGTGCTCC 1989
Db      1922 GCCACACCTTTCGAGTACTGTTGTTGTTCTTCCAAAGACAGCACTGGGTGCTCC 1981
Qy      1990 AGGCTTCTGCTTACAGATTTGCTCTGCACTGACACACCTGCAACCTCTGACAC 2049
Db      1982 AGGCTTCTGCTTACAGATTTGCTCTGCACTGACACACCTGCAACCTCTGACAC 2041
Qy      2050 ACTGACACACCGTCCCTCCCGGACAGAGCCAGAGCACTGCTTGGCTGCTGTC 2109
Db      2042 ACTGACACACCGTCCCTCCCGGACAGAGCCAGAGCACTGCTTGGCTGCTGTC 2101
Qy      2110 TCTTGCATTAAGCTCTAGGCTGAGCTTTCACCCCTCTTCCACCACTCTCTGCCCC 2169
Db      2102 TCTTGCATTAAGCTCTAGGCTGAGCTTTCACCCCTCTTCCACCACTCTCTGCCCC 2161
Qy      2170 CAAAAGTGTCAAGGGGCCCTTAGAAGCTGTAAGCTGTTCTGCTTTTCATTCTGGGTC 2229
Db      2162 CAAAAGTGTCAAGGGGCCCTTAGAAGCTGTAAGCTGTTCTGCTTTTCATTCTGGGTC 2221
Qy      2230 TTTTTCAGAAAGATGAGAGAGAAACATGTCGTGAACTTGATGCTGGAGATGTTAAT 2289
Db      2222 TTTTTCAGAAAGATGAGAGAGAAACATGTCGTGAACTTGATGCTGGAGATGTTAAT 2281
Qy      2290 CAGAAGAGCAAAATTTGCTGAGAGCTCAAGGCTGAGATTGGCAGTGTGGCTCCACGC 2349
Db      2282 CAGAAGAGCAAAATTTGCTGAGAGCTCAAGGCTGAGATTGGCAGTGTGGCTCCACGC 2341
Qy      2350 CCTCTCTCCTCGCTAAGGCTTCCGCTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 2409
Db      2342 CCTCTCTCCTCGCTAAGGCTTCCGCTGAGCTGAGCTGCTGCTGCTGCTGCTGCTGCT 2401
Qy      2410 TCTGGGCTCAACCAAGCCCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2469
Db      2402 TCTGGGCTCAACCAAGCCCTGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCTGAGGCT 2461
Qy      2470 GGAACCTCTGGGGTTTGTGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2529
Db      2462 GGAACCTCTGGGGTTTGTGGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2521
Qy      2530 CAGGGGCGGTCCAGAGAGAGGTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2589
Db      2522 CAGGGGCGGTCCAGAGAGAGGTGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2581
Qy      2590 TGGCAGCGGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2649
Db      2582 TGGCAGCGGCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2641
Qy      2650 GTCAATATAAGTATATTTT 2673
Db      2642 GTCAATATAAGTATATTTT 2665

```

```

RESULT 9
LOCUS   HS1005F21
DEFINITION
          HS1005F21 100976 bp DNA linear PRI 24-APR-2001
          Human DNA sequence from clone RP5-1005F21 on chromosome 20. Contains
          the PSMA7 gene for proteasome subunit 7, alpha type (prosome,
          macropain), the HRH3 gene encoding histamine receptor H3, the
          KIAA0693 gene similar to SSXT (synovial sarcoma, translocated to X
          chromosome), a novel gene for a GTP-binding protein, the 3' end of
          a novel gene similar to Pleurodeles waltl RAPS protein, 7 Cpg
          islands, ESTs, STSs and GSSs, complete sequence.

```

```

ACCESSION AL078633
VERSION   AL078633.32 GI:9408092
KEYWORDS  HTG: Cpg island; GTP-binding protein; histamine receptor; HRH3;
          KIAA0693; macropain; PSMA7; prosome; proteasome; SSXT; synovial
          sarcoma.
SOURCE    Homo sapiens (human)
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 100976)
AUTHORS   Corby, N.
TITLES     Direct Submission
JOURNAL    Submitted (24-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
          CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
          requests: clonerequest@sanger.ac.uk
          On Jul 23, 2000 this sequence version replaced gi:8919366.
          During sequence assembly data is compared from overlapping clones.
          Where differences are found these are annotated as variations
          together with a note of the overlapping clone name. Note that the
          variation annotation may not be found in the sequence submission
          corresponding to the overlapping clone, as we submit sequences with
          only a small overlap as described above.
          The following abbreviations are used to associate primary accession
          numbers given in the feature table with their source databases:
          Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WormPep; Information
          from the WormPep database can be found at
          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
          was generated from part of bacterial clone contigs of human
          chromosome 20, constructed by the Sanger Centre Chromosome 20
          Mapping Group. Further information can be found at
          http://www.sanger.ac.uk/HGP/Chr20
          This sequence is the entire insert of clone RP5-1005F21. The true
          left end of clone RP11-11M20 is at 81766 in this sequence. The true
          right end of clone RP11-157P1 is at 51899 in this sequence. This
          sequence was finished as follows unless otherwise noted: all
          regions were either double-stranded or sequenced with an alternate
          chemistry or covered by high quality data (i.e., phred quality >=
          30); an attempt was made to resolve all sequencing problems, such
          as compressions and repeats; all regions were covered by at least
          one plasmid subclone or more than one M13 subclone; and the
          assembly was confirmed by restriction digest. RP5-1005F21 is from
          the library RPc1-5 constructed by the group of Pieter de Jong. For
          further details see
          http://www.chori.org/bacpac/home.htm
          VECTOR: pCYPAC2.
FEATURES
          source
          location/Qualifiers
          1..100976
          /organism="Homo sapiens"
          /mol_type="genomic DNA"
          /db_xref="taxon:9606"
          /chromosome="20"
          /clone="RP5-1005F21"
          /clone_11b="RPc1-5"
          192..264
          /note="MTR repeat: matches 80..152 of consensus"
          1671..1927
          /note="MTR repeat: matches 137..370 of consensus"
          3036..3149
          /note="MER45 repeat: matches 1..116 of consensus"
          3564..3753
          /note="10 copies 19 mer 92% conserved"
          4978..5037
          /note="6 copies 10 mer agtctgtgtg 78% conserved"
          4981..5036
          /note="4 copies 14 mer 85% conserved"
          5041..5110
          /note="7 copies 10 mer tctgtgtgtg 72% conserved"
          5042..5109
          /note="34 copies 2 mer gt 72% conserved"
          5116
          /note="33 copies 2 mer tg 69% conserved"
          5181..5276
          /note="3 copies 32 mer 78% conserved"

```

repeat_region	5188..5275	/note="4 copies 22 mer 75% conserved"
repeat_region	5190..5269	/note="8 copies 10 mer gtcgtgtgtgt 73% conserved"
repeat_region	5274..5675	/note="201 copies 2 mer tg 59% conserved"
repeat_region	5292..5675	/note="12 copies 32 mer 63% conserved"
repeat_region	5295..5694	/note="8 copies 50 mer 64% conserved"
repeat_region	5341..5439	/note="3 copies 33 mer 96% conserved"
repeat_region	5349..5543	/note="5 copies 39 mer 65% conserved"
repeat_region	5386..5931	/note="26 copies 21 mer 54% conserved"
repeat_region	5407..5678	/note="8 copies 34 mer 66% conserved"
repeat_region	5440..5538	/note="3 copies 33 mer 79% conserved"
repeat_region	5502..5669	/note="7 copies 24 mer 69% conserved"
repeat_region	5507..5676	/note="17 copies 10 mer gtcgtgtgtgt 63% conserved"
repeat_region	5509..5676	/note="12 copies 14 mer 69% conserved"
repeat_region	5640..5787	/note="4 copies 37 mer 77% conserved"
repeat_region	5658..5789	/note="4 copies 33 mer 72% conserved"
repeat_region	5760..5825	/note="33 copies 2 mer gt 71% conserved"
repeat_region	5801..6163	/note="11 copies 33 mer 62% conserved"
repeat_region	5879..5980	/note="3 copies 34 mer 79% conserved"
repeat_region	5931..6176	/note="6 copies 37 mer 72% conserved"
repeat_region	5937..6158	/note="6 copies 37 mer 72% conserved"
repeat_region	5943..6176	/note="6 copies 39 mer 68% conserved"
repeat_region	6128..6199	/note="3 copies 24 mer 84% conserved"
repeat_region	6130..6199	/note="5 copies 14 mer 75% conserved"
repeat_region	6229..6376	/note="4 copies 37 mer 69% conserved"
repeat_region	6333..6652	/note="10 copies 32 mer 67% conserved"
repeat_region	6353..6454	/note="3 copies 34 mer 80% conserved"
repeat_region	6414..6602	/note="9 copies 21 mer 65% conserved"
repeat_region	6433..6492	/note="7 copies 10 mer gggagtggtgt 77% conserved"
repeat_region	6425..6488	/note="37 copies 2 mer gt 74% conserved"
repeat_region	6480..6631	/note="8 copies 19 mer 73% conserved"
repeat_region	6483..6652	/note="5 copies 34 mer 75% conserved"
repeat_region	6852..6903	/note="26 copies 2 mer ca 75% conserved"
repeat_region	6909..6992	/note="6 copies 14 mer 72% conserved"
repeat_region	6910..6989	/note="40 copies 2 mer ac 67% conserved"
repeat_region	7464..7555	/note="46 copies 2 mer gg 62% conserved"
repeat_region	9023..9155	/note="FLNM_C repeat: matches 1..133 of consensus"

```

repeat_region /note="12 repeat: matches 1690. .2509 of consensus"
11214. .13309
/note="LTR16B repeat: matches 356. .452 of consensus"
repeat_region 13076. .13123
/note="MIR repeat: matches 77. .124 of consensus"
repeat_region 14429. .14472
/note="22 copies 2 mer tg 75% conserved"
14611. .16552
/note="Cpg Island"
evidence=not_experimental
repeat_region 15256. .15420
/note="5 copies 3 mer 67% conserved"
repeat_region 15274. .15339
/note="14 copies 9 mer gggggggggc 61% conserved"
15295. .15384
/note="9 copies 10 mer gggggggcggg 67% conserved"
repeat_region 15297. .15396
/note="50 copies 2 mer gg 67% conserved"
15299. .15397
/note="9 copies 11 mer 68% conserved"
repeat_region 15302. .15399
/note="7 copies 14 mer 69% conserved"
15303. .15397
/note="5 copies 19 mer 70% conserved"
repeat_region 15352. .15414
/note="3 copies 21 mer 84% conserved"
15421. .20706
/gene="HRH3"
join(15421. .15955,17019. .17185,18750. .20706)

```

Query Match	72.2%	Score 1949.4	DB 9	Length 100976
Best Local Similarity	98.9%	Pred. No. 4.3e-256		
Matches 1973	Conservative 0	Mismatches 21	Indels 1	Gaps 1
QY 679	CATCAGCTACGACCGCTTCCTGTGTGGTCAACCCGAGCGGTCTATACCGGAGCCGACGAGG	738		
Db 18713	CTTCGCGCCGCCCTGATGACGCTGCCTTTCTGACAGTCTCATACCGGAGCCGACGAGG	18777		
QY 739	TGAACAGCGGGGGGCAATGCGGAAAGATGCTGTGTGTGGGTCTGGCCCTTCTGCTGTGA	798		
Db 18773	TGAACAGCGGGGGGCAATGCGGAAAGATGCTGTGTGTGGGTCTGGCCCTTCTGCTGTGA	18833		
QY 799	CGGACCAAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGAGGCTCCATCCCCGAGGGCCA	858		
Db 18833	CGGACCAAGCCATCCTGAGCTGGGAGTACCTGTCCGGGGGAGGCTCCATCCCCGAGGGCCA	18899		
QY 859	CTGCTATGCGGAGTTCTTTTACAACTGTATCTTCTATACGAGCTTCCACCTCGAGATT	918		
Db 18893	CTGCTATGCGGAGTTCTTTTACAACTGTATCTTCTATACGAGCTTCCACCTCGAGATT	18953		
QY 919	CTTTACGCGCCCTTCCAGCGTCACTCTTAACCTCAGACATGTAACCTGAAACATCCAGAG	978		
Db 18953	CTTTACGCGCCCTTCCAGCGTCACTCTTTAACCCTCAGACATGTAACCTGAAACATCCAGAG	19013		
QY 979	GCGCACCCCGCTTCGCGCTGATGGGGCTCGAGAGGACCGCGGAGCCCGAGGCCCTCCCGCA	1038		



## ORIGIN

TSFWILMANSAVNPVLYPLCHHSFRRAFTKLLCPQKXLIQPHSLHEHCWK"

Query Match 60.6%; Score 1636.2; DB 6; Length 1902;  
Best Local Similarity 88.6%; Pred. No. 4.1e-213;  
Matches 1899; Conservative 0; Mismatches 3; Indels 241; Gaps 2;

QY 530 ATCTCGACTTCTCGTCGCGCGCTTCTGATCCCACTGTATGTATCCCTACGTGCTGACA 589  
DB 1 ATCTCGACTTCTCGTCGCGCGCTTCTGATCCCACTGTATGTATCCCTACGTGCTGACA 60  
QY 590 GGGCCGTGACCTTTCGGCCGGGGCTTGTGAAGCTGTGGTGTGTGTGTGTGTGTGTGTGT 649  
DB 61 GGGCCGTGACCTTTCGGCCGGGGCTTGTGAAGCTGTGGTGTGTGTGTGTGTGTGTGTGT 120  
QY 650 TGCACCTCTCTGCTGCTTCAACATCGTGTATCATAGTACGACGCGCTTCTGTGCGTCAAC 709  
DB 121 TGCACCTCTCTGCTTCAACATCGTGTATCATAGTACGACGCGCTTCTGTGCGTCAAC 180  
QY 710 CGAGCGGTCTCATACCGGCGCCGACGAGGTGACACGCGCGGGCAGTGTGCGAAGATGTG 769  
DB 181 CGAGCGGTCTCATACCGGCGCCGACGAGGTGACACGCGCGGGCAGTGTGCGAAGATGTG 240  
QY 770 CTGT 829  
DB 241 CTGT 300  
QY 830 TCCGGGGGAGCTCCATCCCGGAGGGGCACTGTATGCGAGTCTTCTTACAACTGTATG 889  
DB 301 TCCGGGGGAGCTCCATCCCGGAGGGGCACTGTATGCGAGTCTTCTTACAACTGTATG 360  
QY 890 TTCTCTATCAGCGGCTTCAACCTGTGAGTCTTCAACGCGCTTCTTCAACGCGCTTCTT 949  
DB 361 TTCTCTATCAGCGGCTTCAACCTGTGAGTCTTCAACGCGCTTCTTCAACGCGCTTCTT 420  
QY 950 AACCTCAGATCTTACTGTAAATCCAGAGGCGCACCGGCTTCCGGTGTGTGTGTGTGTGT 1009  
DB 421 AACCTCAGATCTTACTGTAAATCCAGAGGCGCACCGGCTTCCGGTGTGTGTGTGTGTGT 480  
QY 1010 GAGGAGCGCGGCGCCGAGCGCCCTCCGAGGGCCAGACCTTCAACACCCCGACGCGCTGAG 1069  
DB 481 GAGGAGCGCGGCGCCGAGCGCCCTCCGAGGGCCAGACCTTCAACACCCCGACGCGCTGAG 540  
QY 1070 TGCCTGAGGCTGTGTGAGAGAGGAGGCACTGGAGAGGCGCATGCGTGCACAGTATGGAGT 1129  
DB 541 TGCCTGAGGCTGTGTGAGAGAGGAGGCACTGGAGAGGCGCATGCGTGCACAGTATGGAGT 586  
QY 1130 GGTGAGGCGCGGTAGGCGCTGAGGCGGGAGAGGCGACCTTGGGGGTGTGGGTGGGAGC 1189  
DB 587 ----- 586  
QY 1190 GGCTCCGTGGCTTCAACCACTCCAGCTCCGAGGCTCTCGAGGGGCACTGAGAGGCGG 1249  
DB 587 ----- 586  
QY 1250 CGCTCACTCAGAGAGGGGCTCAAGCGGTGCGGCTCTCGCTGAGAGAGGCGCATG 1309  
DB 587 ----- 586  
QY 1310 AAGATGTGTCTCCAGAGCTTCAACCAAGCGCTTTCGAGTGTCTCGGAGACGAAAGTGGCT 1369  
DB 587 -----ACAGGAAAGTGGCT 600  
QY 1370 AAGTCGTGCGCTCATCTGTAGAGCTTCTTGGGCTGTGTGGGCGCCCATACAGCGCTGTG 1429  
DB 601 AAGTCGTGCGCTCATCTGTAGAGCTTCTTGGGCTGTGTGGGCGCCCATACAGCGCTGTG 660  
QY 1430 ATGATCATCCGGGCGCGCTGCATGGCACACTGCTCTCTGACTACTGTGTATCGAAACCTTC 1489  
DB 661 ATGATCATCCGGGCGCGCTGCATGGCACACTGCTCTCTGACTACTGTGTATCGAAACCTTC 720  
QY 1490 TTCTGGCTCTGTGGGCACTCGGCTGTCAACCTGTCTCTTACCTCTTGTGCCACAC 1549

DB 721 TTCTGGCTCTGTGGGCAACTCGGCTGTCAACCTGTCTCTTACCTCTGTGCCACAC 780  
QY 1550 AGCTTCCGCGGGGCGCTTCAACCAAGCTGTCTGCGCCCGACAGAGCTCAAAATCCAGCCCGAC 1609  
DB 781 AGCTTCCGCGGGGCGCTTCAACCAAGCTGTCTGCGCCCGACAGAGCTCAAAATCCAGCCCGAC 840  
QY 1610 AGCTTCCGCGGGGCGCTTCAACCAAGCTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1669  
DB 841 AGCTTCCGCGGGGCGCTTCAACCAAGCTGTCTGAGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
QY 1670 TCTCAGCCCAAGTCTCTGAGGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1729  
DB 901 TCTCAGCCCAAGTCTCTGAGGAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960  
QY 1730 GGGGTGAGGCGCGGCTGT 1789  
DB 961 GGGGTGAGGCGCGGCTGT 1020  
QY 1790 GAGGCGCTTCTCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1849  
DB 1021 GAGGCGCTTCTCTGAGGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
QY 1850 GGGCCCTGCGCCCGACATTTGTGGCTTCAACCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1909  
DB 1081 GGGCCCTGCGCCCGACATTTGTGGCTTCAACCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139  
QY 1910 GCTGCCACCCCGCTGT 1969  
DB 1140 GCTGCCACCCCGCTGT 1199  
QY 1970 CAAGCACTGGGT 2029  
DB 1200 CAAGCACTGGGT 1259  
QY 2030 AACTGCAACCCCGCTGT 2089  
DB 1260 AACTGCAACCCCGCTGT 1319  
QY 2090 TGCCTTGT 2149  
DB 1320 TGCCTTGT 1379  
QY 2150 CCACCACTCTGT 2209  
DB 1380 CCACCACTCTGT 1439  
QY 2210 CTGCTTTTCCATTTCTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2269  
DB 1440 CTGCTTTTCCATTTCTGGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1499  
QY 2270 ATGTCGT 2329  
DB 1500 ATGTCGT 1559  
QY 2330 GAGGAGT 2389  
DB 1560 GAGGAGT 1619  
QY 2390 CTGCTTTTCCACCCCGCTGTGGGCTTCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGT 2449  
DB 1620 CTGCTTTTCCACCCCGCTGTGGGCTTCAACCGGCTGTGTGTGTGTGTGTGTGTGTGTGT 1679  
QY 2450 CCACTCTGT 2509  
DB 1680 CCACTCTGT 1739  
QY 2510 CCGAGGAGT 2569  
DB 1740 CCGAGGAGT 1799  
QY 2570 CGCAGT 2629  
DB 1800 CGCAGT 1859

QY 2630 GCTGCCCTGCAACCGTAGAGTCACATTAAGTATTTTTT 2672  
DB 1860 GCTGCCCTGCAACCGTAGAGTCACATTAAGTATTTTTT 1902

RESULT 11  
BD127248 1902 bp DNA linear PAT 18-SEP-2002  
LOCUS BD127248  
DEFINITION Primer for synthesizing full-length cDNA and use thereof.  
ACCESSION BD127248  
VERSION BD127248.1 GI:23222193  
KEYWORDS JP 2002017375-A/2679.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 1902)  
Oca.T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,  
Makamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and  
Koga,H.  
Primer for synthesizing full-length cDNA and use thereof  
Patent: JP 2002017375-A 2679 22-JAN-2002;  
HELIX RESEARCH INSTITUTE  
OS Homo sapiens (human)  
PN JP 2002017375-A/2679  
PD 22-JAN-2002 JP 2002053172  
PF 07-JUL-2000 JP 2002053172  
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO  
PI ISHII,  
PI YUAI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI  
SHINICHI KOJIMA,  
PI TETSUO OTSUKI,HISASHI KOGA  
PC C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC  
10, C12P21/02,C12O1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC  
Primer for synthesizing full-length cDNA and use thereof FH Key  
Location/Qualifiers  
FT CDS (235)..(864).

FEATURES  
source  
1. 1902  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 60.6%; Score 1636.2; DB 6; Length 1902;  
Best Local Similarity 88.6%; Pred. No. 4,1e-213;  
Matches 1899; Conservative 0; Mismatches 3; Indels 241; Gaps 2;  
QY 530 ATCTCGACTCTCTGTCGGGCGCTTCTGATCCACTGTATGACCTTACGTCGACA 589  
DB 1 ATCTCGACTCTCTGTCGGGCGCTTCTGATCCACTGTATGACCTTACGTCGACA 60  
QY 590 GGGCGCTGACCTTGGCGCGGGCGCTTGTGACGCTGTGGTGTGAGTGACTACCTGCTG 649  
DB 61 GGGCGCTGACCTTGGCGCGGGCGCTTGTGACGCTGTGGTGTGAGTGACTACCTGCTG 120  
QY 650 TGCACCTCTCTGCTTCAACATCGTGTGATCAGCTACGACGCGCTTCTGTCGGTCAAC 709  
DB 121 TGCACCTCTCTGCTTCAACATCGTGTGATCAGCTACGACGCGCTTCTGTCGGTCAAC 180  
QY 710 CGAGCGGTCTCATACCGGGCGCGAGGGTGAACCGCGCGGGCAGTGCAGGAAGTCTG 769  
DB 181 CGAGCGGTCTCATACCGGGCGCGAGGGTGAACCGCGCGGGCAGTGCAGGAAGTCTG 240  
QY 770 CTGGTGTGGGTGCTGGCTTCTGCTGTGACGACACGACATCTTGAAGTGGAGTACTG 829  
DB 241 CTGGTGTGGGTGCTGGCTTCTGCTGTGACGACACGACATCTTGAAGTGGAGTACTG 300  
QY 830 TCCGGGGGAGCTCATCCCGAGGGGCACTGCTATGCGAGTCTTCTTCAACATGCTATC 889

DB 301 TCCGGGGGAGCTCATCCCGAGGGGCACTGCTATGCGAGTCTTCTTCAACATGCTATC 360  
QY 890 TTCTCATACCGGCTTCCACCGGAGTTCTTAAAGCCCTTCTCCAGGCGTCACTTCTT 949  
DB 361 TTCTCATACCGGCTTCCACCGGAGTTCTTAAAGCCCTTCTCCAGGCGTCACTTCTT 420  
QY 950 AACCTGACATCTACCTGAACATCCAGAGGCGGACCGGCTCCGGCTGTATGGGGCTGCA 1009  
DB 421 AACCTGACATCTACCTGAACATCCAGAGGCGGACCGGCTCCGGCTGTATGGGGCTGCA 480  
QY 1010 GAGGACGCGGCGCGGAGCGGCTTCCGAGGCGGAGGCGGAGGCTTCCAGCGGCTGCG 1069  
DB 481 GAGGACGCGGCGGAGCGGCGGCTTCCGAGGCGGAGGCGGAGGCTTCCAGCGGCTGCG 540  
QY 1070 TGCTGGGGGCTGTGCGAGGAAGGGGCAACGGGAGGCGGAGGCTTCCAGGCTATGGGGTG 1129  
DB 541 TGCTGGGGGCTGTGCGAGGAAGGGGCAACGGGAGGCGGAGGCTTCCAGGCTATGGGGTG 586  
QY 1130 GGTGAGGCGGCGGTAGGCGGCTGAGGCGGAGGCGGAGGCGGAGGCTTCCAGGCTATGGGGTG 1189  
DB 587 ----- 586  
QY 1190 GGTCCGCGGCTTCAACCACTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1249  
DB 587 ----- 586  
QY 1250 CGCTCACTAAGAGGGGCTCAAGCGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGGATG 1309  
DB 587 ----- 586  
QY 1310 AAGATGATGCCAGAGCTTCAACCAAGCGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1369  
DB 587 ----- 586  
QY 1370 AAGTCCGCGGCGCTTCAACCAAGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1429  
DB 601 AAGTCCGCGGCGCTTCAACCAAGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 660  
QY 1430 ATGATATCCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1489  
DB 661 ATGATATCCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 720  
QY 1490 TTCTGCTCTGTCGGGCGGCACTGCGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1549  
DB 721 TTCTGCTCTGTCGGGCGGCACTGCGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 780  
QY 1550 AGCTTCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1609  
DB 781 AGCTTCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 840  
QY 1610 AGCTTCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1669  
DB 841 AGCTTCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 900  
QY 1670 TCTCAGCCCAAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1729  
DB 901 TCTCAGCCCAAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 960  
QY 1730 GGGGTGAGCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1789  
DB 961 GGGGTGAGCGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1849  
QY 1790 GAGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1849  
DB 1021 GAGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1808  
QY 1850 CGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1909  
DB 1081 CGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1139  
QY 1910 GGTGCCCAAGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1969  
DB 1140 GGTGCCCAAGCGGCGGCTTCCAGGCTTCCAGGCTTCCAGGCTTCCAGGCGGCACTGAGAGGCGG 1199

Qy	1970	CAAGCACTGGGGTGGCTCCAGGGCTCCCTGGCCCTAGAGATTGGCTCTGCACGTGCAC	2029
Db	1200	CAAGCACTGGGGTGGCTCCAGGGCTCCCTGGCCCTAGAGATTGGCTCTGCACGTGCAC	1259
Qy	2030	ACCTGCACACCCCTGCACACACCTGCACACCGCTCTCTCCCGGACAGCCACAGACAC	2089
Db	1260	ACCTGCACACCCCTGCACACACCTGCACACCGCTCTCTCCCGGACAGCCACAGACAC	1319
Qy	2090	TGCCTTTGGCTGGCTTGTGTCTCTTGGCATAACCTTCAGGCCCTGGCCCTTTACCCCTCTTC	2149
Db	1320	TGCCTTTGGCTGGCTTGTGTCTCTTGGCATAAACCTTCAGGCCCTGGCCCTTTTACCCCTCTTC	1379
Qy	2150	CCACCAACTCTCTCTGCCCCCCCCAAAAGTGTCAAGGGGCCCTAGGAACCTCGAAGCTGTCT	2209
Db	1380	CCACCAAGTCTCTCTGCCCCCCCCAAAAGTGTCAAGGGGCCCTAGGAACCTCGAAGCTGTCT	1439
Qy	2210	CTGCTTTTCATCTCTGGGTGTCTTTCAGAAAGATGAGAGAAAATCATGTCTGTGAACCTG	2269
Db	1440	CTGCTTTTCATCTCTGGGTGTCTTTCAGAAAGATGAGAGAAAATCATGTCTGTGAACCTG	1499
Qy	2270	ATGTTTCGTGGGATGTTTAAATCAAGAGACAAAATGTCTAGAGACTCAAGGCTGGATGG	2329
Db	1500	ATGTTTCGTGGGATGTTTAAATCAAGAGACAAAATGTCTAGAGACTCAAGGCTGGATGG	1559
Qy	2330	GCAGGTGGGGCTCCACAGCCCTCTCCCTCCGCTAAGGCTTCCGGCTGAGCTGTGCAG	2389
Db	1560	GCAGGTGGGGCTCCACAGCCCTCTCCCTCCGCTAAGGCTTCCGGCTGAGCTGTGTGACG	1619
Qy	2390	CTGCTTTCTGCCACCCCGCTCTTGGGGCTCACACCAAGCCCTGTGGCCAAAGCTTGTCCCGG	2449
Db	1620	CTGCTTTCTGCCACCCCGCTCTTGGGGCTCACACCAAGCCCTGTGGCCAAAGCTTGTCCCGG	1679
Qy	2450	CCACTCTGTTGTCTCACACCAAGACCTCTGGGGGTGTGTTGGAGAGAGGGGGGCCCGCTGGG	2509
Db	1680	CCACTCTGTTGTCTCACACCAAGACCTCTGGGGGTGTGTTGGAGAGAGGGGGGCCCGCTGGG	1739
Qy	2510	CCCGAGGGTCCCAAGGCGGTGACGGGGCGGTCCAGAGAGGTGCCCGGCGAAGGGCCGCTT	2569
Db	1740	CCCGAGGGTCCCAAGGCGGTGACGGGGCGGTCCAGAGAGGTGCCCGGCGAAGGGCCGCTT	1799
Qy	2570	CGCCATGTGTCTGTGCAACCGTGGCCACGCGCTCTGTGATCTCTCTGTGCTGTGGCCCGCTGC	2629
Db	1800	CGCCATGTGTCTGTGCAACCGTGGCCACGCGCTCTGTGATCTCTCTGTGCTGTGGCCCGCTGC	1859
Qy	2630	GCTGCGCCCTGCACAAACCGTAGGGTCACATTAAGTGTATTTTTT	2672
Db	1860	GCTGCGCCCTGCACAAACCGTAGGGTCACATTAAGTGTATTTTTT	1902
RESULT 12			
LOCUS	AK074730		
DEFINITION	Homo sapiens cDNA FLJ90249 fis, clone NT2RM2001941, weakly similar to MUSCARINIC ACETYLCHOLINE RECEPTOR M1.		
ACCESSION	AK074730		
VERSION	AK074730.1	GI:22760362	
KEYWORDS	oligo capping; fis (full insert sequence).		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Naganari,K., Maeno,Y., Ono,T., Okano,K., Yoshikawa,Y., Aocsa,S., Sasaki,N., Hatтори,A., Okumura,K., Iwayanagi,T. and Niinomiya,K.		
TITLE	NEDO human cDNA sequencing project		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1902)		
AUTHORS	Isogai,T. and Otsuki,T.		

COMMENT	FEATURES	source
TITLE JOURNAL	Direct Submission Submitted (25-MAR-2002) Takao Isegai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan (E-mail:genomic@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)	
	NEBO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology; cDNA library construction; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.).	
	Location/Qualifiers	
	1..1902	
	/organism="Homo sapiens"	
	/mol_type="mRNA"	
	/db_xref="taxon:9606"	
	/clone="NT2RM2001941"	
	/cell_line="NT2"	
	/cell_type="teratocarcinoma"	
	/note="cloning vector: pME18SFL3-mRNA from uninduced NT2 neutonal precursor cells"	
	235..867	
	/note="unnamed protein product"	
	/codon_start=1	
	/protein_id="BAC1167.1"	
	/db_xref="gi:22760363"	
	/translation="MLLVWYIALPLVGPALISWEVYLSSGSSIPDEGHVAFPNWYFL ITNSTLEETPFPLSVTFPNLSYINIORRLRLDGRREAGPEPPPEADSPSPPPG CWGCMQKGHEAMPLEHRKAKSLAIVISITGLCMAPYTLMLITRAACHGCVDPWYE TSFWLLMANSANVPVLYPLCHHSFRFAFTLCPQKLKIOPHSLSEHCWK"	
ORIGIN		
Query Match	60.6%; Score 1636.2; DB 9; Length 1902;	
Best Local Similarity	88.6%; Pred. No.4.1e-213;	
Matches 1899; Conservative	0; Mismatches 3; Indels 241; Gaps 2;	
OY	530 ATCTCCACATCTCCCTGCTGCGGCGCTTCTTGATCCCACTGATGATACCTTACGCTGACCA 589	
Db	1 ATCTCCACATCTCCCTGCTGCGGCGCTTCTTGATCCCACTGATGATACCTTACGCTGACCA 60	
OY	590 GGCCTGCTGACCTTTCGGCGCGGCGCTTCTGCAAGCTGTGGCTGGTATGATGACTTACTGTCTG 649	
Db	61 GGCCTGCTGACCTTTCGGCGCGGCGCTTCTGCAAGCTGTGGCTGGTATGATGACTTACTGTCTG 120	
OY	650 TGCACTCTCTGCTGCTTCAACATAGTGTCTATCATGACTAGACAGACGCTTCCGTGCGATCACC 709	
Db	121 TGCACTCTCTGCTGCTTCAACATAGTGTCTATCATGACTAGACAGACGCTTCCGTGCGATCACC 180	
OY	710 CGACCGGTCTCATACCGGCGCCACAGACAGGTGACACGCGCGGCGGACGTGCGGAAATGCTG 769	
Db	181 CGACCGGTCTCATACCGGCGCCACAGACAGGTGACACGCGCGGCGGACGTGCGGAAATGCTG 240	
OY	770 CTGGTGTGGGTGCTGCGCTTCTGCTGTACGACCAAGCATCTTGAGCTGGGAATACCTG 829	
Db	241 CTGGTGTGGGTGCTGCGCTTCTGCTGTACGACCAAGCATCTTGAGCTGGGAATACCTG 300	
OY	830 TCCGGGGGAGACTCATATCCCGAGAGGACCACTGATGCGAGTCTTCTTACAACTGGTATC 889	
Db	301 TCCGGGGGAGACTCATATCCCGAGAGGACCACTGATGCGAGTCTTCTTACAACTGGTATC 360	
OY	890 TTCTCTATCAAGCGCTTCCACCTCGAGATTCTTTAAGCGCTTCTCAAGCGTCACTTCTTT 949	
Db	361 TTCTCTATCAAGCGCTTCCACCTCGAGATTCTTTAAGCGCTTCTCAAGCGTCACTTCTTT 420	
OY	950 AACCTCAGCATCTTACCTGGAACATCAAGAGGCGACCCGCTTCCGGCTGGATGGGGCTTCGA 1009	
Db	421 AACCTCAGCATCTTACCTGGAACATCAAGAGGCGACCCGCTTCCGGCTGGATGGGGCTTCGA 480	
OY	1010 GAGCGAGCGGGCCCCGAGCGCCCTTCCGAGGCCCCAGGCGCTTACACACCCCAACCGCTTGGC 1069	
Db	481 GAGCGAGCGGGCCCCGAGCGCCCTTCCGAGGCCCCAGGCGCTTACACACCCCAACCGCTTGGC 540	



1070 TCTGGGGGCTGTGTGAGAGAGGGGCAAGGGGAGCCATGCGCTGACAGATATGGGGT 1129  
541 TCTGGGGGCTGTGTGAGAGAGGGGCAAGGGGAGCCATGCGCTGCGTGC----- 586  
1130 GGTGAGGCGGCGGTAGGCGCTGAGGCGGAGGAGCACTCTGAGGGGTGGCGGTGGGAGC 1189  
587 ----- 586  
1190 GGCTCCGTGGCTTACCCACCTCCAGCTCCGCGAGCTCTCGAGAGGGGCACTGAGAGGCCG 1249  
587 ----- 586  
1250 CGCTCACTCAAGAGAGGGGCTCAAGCGGTGCGTCTCGGCGCTCGCTGAGAGAGCGCATG 1309  
587 ----- 586  
1310 AAGATGTTGTCCAGAGCTTACCCAGCGCTTTCGCTGTCTTGAGGACAGAGAAAGTGGCC 1369  
587 -----ACAGAGAAAGTGGCC 600  
1370 AAGTCCGTGGCCGCTCATTCGTGAGCATTTTGGGCTGTGCTGGGCCCCCATACAGCTGCTG 1429  
601 AAGTCCGTGGCCGCTCATTCGTGAGCATTTTGGGCTGTGCTGGGCCCCCATACAGCTGCTG 660  
1430 ATGATCATCCGGGCGGCTGAGCACTGAGCACTGAGTCCCTGACTGATGATGAGAAACCTCC 1489  
661 ATGATCATCCGGGCGGCTGAGCACTGAGCACTGAGTCCCTGACTGATGATGAGAAACCTCC 720  
1490 TTCTGGCTCTGTGGGCAACTGGGCTGTCAACCTGTCTCTTAACTGATGATGAGCACTG 1549  
721 TTCTGGCTCTGTGGGCAACTGGGCTGTCAACCTGTCTCTTAACTGATGATGAGCACTG 780  
1550 AGCTTCCGCGGGGCTTCAACAGAGCTGCTGCGCCCAAGAGTCAAAATCCAGGCCAC 1609  
781 AGCTTCCGCGGGGCTTCAACAGAGCTGCTGCGCCCAAGAGTCAAAATCCAGGCCAC 840  
1610 AGCTCCCTGGAGACATGCTGGAAGTGAAGGCGCCACAGAGCTCCCTCAAGCCAGCCCTC 1669  
841 AGCTCCCTGGAGACATGCTGGAAGTGAAGGCGCCACAGAGCTCCCTCAAGCCAGCCCTC 900  
1670 TCTCAGCCCAAGGCTCTCTGGGCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1729  
901 TCTCAGCCCAAGGCTCTCTGGGCACTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
1730 GGGGTGAGCGCCGCGGTGTCTGTGCGCTCTTAAATGCCAGCGGAGCCAGCTGCGCATG 1789  
961 GGGGTGAGCGCCGCGGTGTCTGTGCGCTCTTAAATGCCAGCGGAGCCAGCTGCGCATG 1020  
1790 GAGGGGCGCTTCTGTGGGTTGGCCAGAGGGCGCCCTCACTGCTGAGCTGAGAGGCTGGGTC 1849  
1021 GAGGGGCGCTTCTGTGGGTTGGCCAGAGGGCGCCCTCACTGCTGAGCTGAGAGGCTGGGTC 1080  
1850 CGGCGCTGCGCCCAATTTGTGCTCAGCGGAGGAGGAGAGTCTGAGAGGCTCCAGACAT 1909  
1081 CGGCGCTGCGCCCAATTTGTGCTCAGCGGAGGAGGAGTCTGAGAGGCTCCAGACAT 1139  
1910 GCTGCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1969  
1140 GCTGCCACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1199  
1970 CAAGGACCTGGGTTGCTCAGAGCTTCCGCGCTTACAGATTTGCTCTGAGAGTGTGACAC 2029  
1200 CAAGGACCTGGGTTGCTCAGAGCTTCCGCGCTTACAGATTTGCTCTGAGAGTGTGACAC 1259  
2030 AACTGACACCCCTGACACACTGTGACACCGTCCCTCTCCCGGAGCAAGCCAGAGACAC 2089  
1260 AACTGACACCCCTGACACACTGTGACACCGTCCCTCTCCCGGAGCAAGCCAGAGACAC 1319  
2090 TGGCTTGTGCTGCTTGTGTCTGTGATTAAGCTTCAAGGCTGAGCTTCAAGCTTCTTC 2149  
1320 TGGCTTGTGCTGCTTGTGTCTGTGATTAAGCTTCAAGGCTGAGCTTCAAGCTTCTTC 1379  
2150 CCACCAACTCTCTCTGCGCCCAAAAGTGTCAAGGGGCGCTGAGAACCTGGAAGCTTCT 2209

1380 CCACGAGCTCTCTGCGCCCAAAAGTGTCAAGGGGCGCTGAGAACCTGGAAGCTGTTCT 1439  
2210 CTGCTTTTCATTTCTGGGTTTTCAGAAAGATGAAGAAAGAAACATGCTGTGAACCTG 2269  
1440 CTGCTTTTCATTTCTGGGTTTTCAGAAAGATGAAGAAAGAAACATGCTGTGAACCTG 1499  
2270 ATGTTCTGGGATGTTTAAATCAAGAGAGCAAAATGCTGAGAGCTCAAGGCTGAGATTG 2329  
1500 ATGTTCTGGGATGTTTAAATCAAGAGAGCAAAATGCTGAGAGCTCAAGGCTGAGATTG 1559  
2330 GAGAGTGTGGGCTCCACGCGCCCTCTCCCTCGCTTAAGGCTTCCGCTGAGCTGTGCGAG 2389  
1560 GAGAGTGTGGGCTCCACGCGCCCTCTCCCTCGCTTAAGGCTTCCGCTGAGCTGTGCGAG 1619  
2390 CTGCTTTCTGCGCCACCGGCTCTGAGGCTCAACAGAGCTGAGGCTGAGGCTGAGGCTG 2449  
1620 CTGCTTTCTGCGCCACCGGCTCTGAGGCTCAACAGAGCTGAGGCTGAGGCTGAGGCTG 1679  
2450 CCACTGTTGTTGCTACCCAGAGACCTTGGGGGTTGTTGGAGAGAGGGGCGCGCTGAG 2509  
1680 CCACTGTTGTTGCTACCCAGAGACCTTGGGGGTTGTTGGAGAGAGGGGCGCGCTGAG 1739  
2510 CCGAGAGGTCCTCAAGGCGTGTGAGAGGGGCGGTCCAGAGAGAGTGTGCGGAGAGGGGCGCTT 2569  
1740 CCGAGAGGTCCTCAAGGCGTGTGAGAGGGGCGGTCCAGAGAGAGTGTGCGGAGAGGGGCGCTT 1799  
2570 CCGCATGCTGTGTGACACCGGCTGACAGCGGCTGTGATGCTCTGCTGCTGCTGCTGCTG 2629  
1800 CCGCATGCTGTGTGACACCGGCTGACAGCGGCTGTGATGCTCTGCTGCTGCTGCTGCTG 1859  
2630 GCTGCGCTGCAAAACGTGAGGTCAACAATAAGTATTTT 2672  
1860 GCTGCGCTGCAAAACGTGAGGTCAACAATAAGTATTTT 1902

RESULT 13  
E39817  
LOCUS  
DEFINITION  
E39817 Novel guanosine triphosphate (GTP)-binding protein-conjugate receptor protein.  
ACCESSION  
E39817  
VERSION  
E39817.1 GI:18627098  
KEYWORDS  
UP 2000189171-A/12.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
REFERENCE  
Itaya,K., Takimura,T., Nakamura,T., Kobayashi,M., Tana,K., Hida,K., Y. and Ota,M.  
TITLE  
Novel guanosine triphosphate (GTP)-binding protein-conjugate receptor protein  
JOURNAL  
Patent: JP 2000189171-A 12 11-JUL-2000;  
BANYU PHARMACEUT CO LTD  
COMMENT  
OS Homo sapiens (human)  
PN UP 2000189171-A/12  
PD 11-JUL-2000  
PF 25-MAY-1999 JP 1999145661  
PR 25-DEC-1998 WO PCTJP9805967  
PI KEI ITAYA, TETSUO TAKIMURA, TAKAO NAKAMURA, MASAHIKO KOBAYASHI, PI KENICHI TANAKA,  
PI YOSUKE HIDAKA, MASAKI OTA  
PC C12N15/09, A61K45/00, C07K14/705, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,  
PC C12P21/02, C12Q1/02, G01N33/15, G01N33/566, C12N15/00, C12N5/00 CC

FEATURES  
source  
FH Key Location/Qualifiers  
FT exon Location/Qualifiers  
1..1893  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

ORIGIN

/db\_xref="taxon:9606"

Query Match 58.9%; Score 1590.2; DB 6; Length 1893;

Best Local Similarity 98.5%; Pred. No. 7.4e-207; Mismatches 23; Indels 1; Gaps 1;

Matches 1615; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

QY 679 CATCAGCTACGACCGCTTCTGTGCTCAACCCGAGCGTCTCATACCGGAGCCGACAGAGG 738  
DB 256 CTTCCGCCCCCGGCTTGACAGCGCTGCTCTTGCTGAGCTCTCATACCGGAGCCGACAGAGG 315  
QY 739 TGAACAGCGCGGCGGAGCTGCGGAAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 798  
DB 316 TACACAGCGCGGCGGAGCTGCGGAAAGTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 375  
QY 799 CGGACAGCGCATCTCTAGCTGGGAGTACCTGTCCGAGGCGAGCTCCATCCCGAGGAGGCA 858  
DB 376 CGGACAGCGCATCTCTAGCTGGGAGTACCTGTCCGAGGCGAGCTCCATCCCGAGGAGGCA 435  
QY 859 CTGCTATGCGAGTCTTCTTACAACTGTACTTCTCATACCGGCTTCCAGCTTGAAGTT 918  
DB 436 CTGCTATGCGAGTCTTCTTACAACTGTACTTCTCATACCGGCTTCCAGCTTGAAGTT 495  
QY 919 CTTTACGCGCTTCTCTAGGCTCACTTCTTTAACTCTAGATTTACTTGAATCTCCAGAG 978  
DB 496 CTTTACGCGCTTCTCTAGGCTCACTTCTTTAACTCTAGATTTACTTGAATCTCCAGAG 555  
QY 979 GCGACACCGCTCTCGGCTGGATGGGCTGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGG 1038  
DB 556 GCGACACCGCTCTCGGCTGGATGGGCTGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGG 615  
QY 1039 GCGCCAGCGCTCAACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098  
DB 616 GCGCCAGCGCTCAACCCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675  
QY 1099 GGAAGCGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1158  
DB 676 GGAAGCGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 735  
QY 1159 GGAAGCGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218  
DB 736 GGAAGCGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795  
QY 1219 CGGACAGCTCTCTGAGGAGGCACTGAGAGCGCGCTCACTCAAGAGGAGCTTCCAGCGC 1278  
DB 796 CGGACAGCTCTCTGAGGAGGCACTGAGAGCGCGCTCACTCAAGAGGAGCTTCCAGCGC 855  
QY 1279 GCGCTCTCTGCGCTCGCTGGAAGAGCGCATGAAGTGTGTCTCCAGAGCTTCCAGCGC 1338  
DB 856 GCGCTCTCTGCGCTCGCTGGAAGAGCGCATGAAGTGTGTCTCCAGAGCTTCCAGCGC 915  
QY 1339 CTTTCCGCTGTCTCGGAGACGAGAAAGTGGCAAGTGGCGCTGCTCATCGTGAAGATCTT 1398  
DB 916 CTTTCCGCTGTCTCGGAGACGAGAAAGTGGCAAGTGGCGCTGCTCATCGTGAAGATCTT 975  
QY 1399 TGGGCTCTGCTGAGGCGCCATACAGCGTGTGATGATCATCGGAGCGGCTTCCAGCGC 1458  
DB 976 TGGGCTCTGCTGAGGCGCCATACAGCGTGTGATGATCATCGGAGCGGCTTCCAGCGC 1035  
QY 1459 CTGCGTCTCTGACTACTGTGTAAGAACTCTCTTGTGCTCTGTGGGCGCACTCGGCTGT 1518  
DB 1036 CTGCGTCTCTGACTACTGTGTAAGAACTCTCTTGTGCTCTGTGGGCGCACTCGGCTGT 1095  
QY 1519 CAACCGTCTCTCTACCTCTGTGCAACAAGCTTCCGCGGCGGCTTCCAGCGC 1578  
DB 1096 CAACCGTCTCTCTACCTCTGTGCAACAAGCTTCCGCGGCGGCTTCCAGCGC 1155  
QY 1579 CTGCGCCGAGAGCTCAAAATCCAGGCCCAAGCTCTCTGAGACACTGTCTGAAGTGA 1638  
DB 1156 CTGCGCCGAGAGCTCAAAATCCAGGCCCAAGCTCTCTGAGACACTGTCTGAAGTGA 1215  
QY 1639 GCGCCACAGAGCTCTCTGAGCAAGCTCTCTCAAGCCAGGCTCTTGGGATGTGCG 1698

DB 1216 GCGCCACAGAGCTCTCTCAAGCCAGGCTCTCTCAAGCCAGGCTCTCTGAGCATGTGCGC 1275  
QY 1699 CCTGTGCGCCCTTACCCGAGCTGTGTCCGCAAGGAGTGAAGCCCGCGCTGTGTGAGCCCT 1758  
DB 1276 CCTGTGCGCCCTTACCCGAGCTGTGTCCGCAAGGAGTGAAGCCCGCGCTGTGTGAGCCCT 1335  
QY 1759 CTTTAAATGCAAGGAGCAAGCTTGTGCAATGAGAGCGCTTCTGTGCTTGTGCAAGAGG 1818  
DB 1336 CTTTAAATGCAAGGAGCAAGCTTGTGCAATGAGAGCGCTTCTGTGCTTGTGCAAGAGG 1395  
QY 1819 CCTGACATGAGGAGCTGAGAGGCTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1878  
DB 1396 CCTGACATGAGGAGCTGAGAGGCTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1455  
QY 1879 CGGAGAGGAGCAAGTGTGAGAGTCCGAGACATGCTGCCACCCCTGTGCTGAGCCCACT 1938  
DB 1456 C-GGAGAGGAGCAAGTGTGAGAGTCCGAGACATGCTGCCACCCCTGTGCTGAGCCCACT 1514  
QY 1939 TGGCAGTTACTGTGTGTGTGTCTTCCCAAAGCAAGCACTGGGTGTGCTCCAGGCTTCT 1998  
DB 1515 TGGCAGTTACTGTGTGTGTGTCTTCCCAAAGCAAGCAAGCTGGGTGTGCTCCAGGCTTCT 1574  
QY 1999 GCGCTAGAGGTTGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2058  
DB 1575 GCGCTAGAGGTTGCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1634  
QY 2059 CCGTCCCTCTCCCGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2118  
DB 1635 CCGTCCCTCTCCCGGAGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1694  
QY 2119 AGCTTCAGGCTGAGGCTTCTTCAAGGCTTCTTCCCAAGGCTTCTTCTGCTGCTGCTGCT 2178  
DB 1695 AGCTTCAGGCTGAGGCTTCTTCAAGGCTTCTTCCCAAGGCTTCTTCTGCTGCTGCTGCT 1754  
QY 2179 CAAGGGGCGCTGAGAAAGCTGCAAGGCTTCTGCTGCTTCTTCAAGGCTTCTTCTGCTGCT 2238  
DB 1755 CAAGGGGCGCTGAGAAAGCTGCAAGGCTTCTGCTGCTTCTTCAAGGCTTCTTCTGCTGCT 1814  
QY 2239 AGATGAGAGAGAAACATGTCTGTGAAGTGTGTGCTGAGATGTTTAAATCAAGAGAGA 2298  
DB 1815 AGATGAGAGAGAAACATGTCTGTGAAGTGTGTGCTGAGATGTTTAAATCAAGAGAGA 1874  
QY 2299 CAAAATTGCTGAGAGCTC 2317  
DB 1875 CAAAATTGCTGAGAGCTC 1893  
  
RESULT 14  
ARS59681 1893 bp DNA linear PAT 08-OCT-2004  
LOCUS ARS59681  
DEFINITION Sequence 13 from patent US 6750322.  
ACCESSION ARS59681  
VERSION ARS59681.1 GI:53969737  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
REFERENCE Unclassified.  
1 (bases 1 to 1893)  
AUTHORS Itadani,H., Takimura,T., Nakamura,T., Kobayashi,M., Tanaka,K.-I.,  
Hidaka,Y. and Ohwa,M.  
TITLE Guanosine triphosphate (GTP) binding protein-coupled receptor  
proteins  
JOURNAL Patent: US 6750322-A 13 15-JUN-2004;  
FEATURES Location/Qualifiers  
source 1..1893  
/organism="unknown"  
/mol\_type="genomic DNA"  
  
ORIGIN  
Query Match 58.9%; Score 1590.2; DB 6; Length 1893;  
Best Local Similarity 98.5%; Pred. No. 7.4e-207;  
Matches 1615; Conservative 0; Mismatches 23; Indels 1; Gaps 1;

[illegible]

Db	1336	CTCTTAATGCGCAGGCAAGCCACCTGCTGACATGAGAGGCGCCCTTCTCGGGTTGGCCAGAGGCG	1395
OY	1819	CCCTCACTGAGCTGAGACTGAGAGGCTGGGTGGCGCGGCCCTGCGCCCCCAATTCCTGAGCTCCAC	1878
Db	1396	CCCTCACTGAGCTGAGAGGCTGAGAGGCTGGCGCGGCCCTGCGCCCCCAATTCCTGAGCTCCAC	1455
OY	1879	CGGGAGAGGAGCAGTCTGAGAGGTGCCAGACATGCTGCCACCCCTGCTGGTGCCACCT	1938
Db	1456	C-GGAGAGGAGCAGTCTGAGAGGTGCCAGACATGCTGCCACCCCTGCTGGTGCCACCT	1514
OY	1939	TGCGAGTTACTGCTGGTTGGTGTCTTCCCAAGCAAGCACTGGGTGTCTCAAGCTTCC	1998
Db	1515	TGCGAGTTACTGCTGGTTGGTGTCTTCCCAAGCAAGCACTGGGTGTCTCAAGCTTCC	1574
OY	1999	GGCCTAGAGTTGCCCTCTGACGTGTGACACACTGTGACACCCCTGTGACACACTGTGAC	2058
Db	1575	GGCCTAGAGTTGCCCTCTGACGTGTGACACACTGTGACACCCCTGTGACACACTGTGAC	1634
OY	2059	CCGTCCCTCTCCCGGGAACAAGCCAGGACACTGCGCTTGTGCTGTGATCTCTTGAT	2118
Db	1635	CCGTCCCTCTCCCGGGAACAAGCCAGGACACTGCGCTTGTGCTGTGATCTCTTGAT	1694
OY	2119	AGCCTCAGGCTGAGCCCTTTCACCCCTTTCACCAACAATCTCTTGCAGCCCCCAAAAGTGT	2178
Db	1695	AGCCTCAGGCTGAGCCCTTTCACCCCTTTCACCAACAATCTCTTGCAGCCCCCAAAAGTGT	1754
OY	2179	CAAGGGGCGCTAGGAACCTGGAAGCTGTCTCTGCTTTCATCTGGGTGTTTCAGAA	2238
Db	1755	CAAGGGGCGCTAGGAACCTGGAAGCTGTCTCTGCTTTCATCTGGGTGTTTCAGAA	1814
OY	2239	AGATGAAGAAAGAAAACATGTCTGTGAACCTTGATGTTGTGTGGATGTTTAATCAAGAGAGA	2298
Db	1815	AGATGAAGAAAGAAAACATGTCTGTGAACCTTGATGTTGTGTGGATGTTTAATCAAGAGAGA	1874
OY	2299	CAAAATGCTGAGGAGCTC 2317	
Db	1875	CAAAATGCTGAGGAGCTC 1893	

```

RESULT 15
LOCUS      AY231164                               1600 bp    mRNA    linear    PRI 19-MAR-2003
DEFINITION Macaca mulatta histamine receptor H3 (HRH3) mRNA, complete cds.
ACCESSION  AY231164
VERSION     AY231164.1  GI:29124990
KEYWORDS
SOURCE      Macaca mulatta (rhesus monkey)
ORGANISM    Macaca mulatta
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
            Cercopithecinae; Macaca.
REFERENCE   1  (bases 1 to 1600)
AUTHORS    Yao,B.B., Sharma,R., Cassar,S., Espenshade,T.A. and Hancock,A.A.
TITLE      Cloning and Pharmacological Characterization of the Monkey
            Histamine H3 Receptor
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 1600)
AUTHORS    Cassar,S., Espenshade,T.A., Hancock,A.A. and Yao,B.B.
TITLE      Direct Submission
JOURNAL     Submitted (07-FEB-2003) R-4MN, Abbott Laboratories, AP9A, 100
            Abbott Park Road, Abbott Park, IL 60064, USA
FEATURES
            location/Qualifiers
            1..1600
            /organism="Macaca mulatta"
            /mol_type="mRNA"
            /db_xref="taxon:9544"
            1..1600
            /gene="HRH3"
            122..1459
            /gene="HRH3"
            /note="G protein-coupled receptor"
            /codon_start=1

```

```

/product="histamine receptor H3"
/protein_id="AA063757.1"
/db_xref="GI:29124991"
/translation="MERAPDGPPLNAGSLAGEAAGAGFSAAMTVALAAMAL
IVATLGNALVLAFAVADSLFTONNPLINLAISDPLVAGACTPLVYPVLTGWT
GRGLKMLVVDYLLCTSSAFVILVLSIDRFLSTRAVAYSRAQGTTRAAKMLLV
VLAFLVGPALISWEYLSGSSIPESHCAEFVFWYPLITSLTEPLPPLSVTFN
LSIYINIGRTRLRDARBAEPAPPPAPQPPPPPCMCWCKGHEANPLRHYG
VGEAAGABAGETALGGGGGSAASPSSSSSRGTERPSLRKSGSSASABLE
KMKRWSSQFTORFLSRDKRVKSLAVSVIFGLCMAPYTLMTIIRACHCHVDPY
MYETSPWILMANSAPVLYPLCHSPFRAPFKLCPQKLQPHSSLEQCMK"

```

## ORIGIN

```

Query Match      55.1%; Score 1486.6; DB 9; Length 1600;
Best Local Similarity 95.9%; Pred. No. 9.4e-193;
Matches 1536; Conservative 0; Mismatches 64; Indels 1; Gaps 1;

```

```

QY 177 GGAAACCCGACCCGCGCAAGGGCCGCGCAAAAGACAGAGGCTCCGGGCGGGGCGCCCTCCCG 236
DB 1 GGAAACCCGACCCGCGCAAGGGCCGCGCAAAAGACAGAGGCTCCGGGCGGGGCGCCCT-CCG 59
QY 237 GCGGCCAGCTCTCGGCGCGCGCGCCCTGCGCCGCGGTCCGGAGCCGCGGTAGCGCTGGGGG 296
DB 60 GCGGCCAGCTCTCGACTGCGCGCCCTGCGCCGCGGTCCGGAGCCGCGGTAGCGCTGGGGG 119
QY 297 CCATGAGAGCGCGCGCGCCGCGCAAGCGCGCTGAAAGCTTCGGGGGCGCTGGCGGGGAGT 356
DB 120 CCATGAGAGCGCGCGCGCCGCGCAAGCGCGCTGAAAGCTTCGGGGGCGCTGGCGGGGAG 179
QY 357 CGGGCGCGCGCGCGCGCGCGCGCGCTTCGGGAGAGCCGCGGTGGCGCGCGCGCGCGCG 416
DB 180 CAGCGCGCGCGCGCGCGCGCGCGCGCTTCGGGAGAGCCGCGGTGGCGCGCGCGCGCGCG 239
QY 417 TCATGAGCGCTGCTCATGCTGAGCGACGCTGAGGCAACGCGTGGTGCATGCTCGCCTTG 476
DB 240 TCATGAGCGCTGCTCATGCTGAGCGACGCTGAGGCAACGCGTGGTGCATGCTCGCCTTG 299
QY 477 TGGCGGACTCGAGCTTCGCGACCCAGAACCAACTTCTTCGTGCTCAACCTTGCGCATTCG 536
DB 300 TGGCGGACTCGAGCTTCGCGACCCAGAACCAACTTCTTCGTGCTCAACCTTGCGCATTCG 359
QY 537 ACTTCTGCTGCGCGCGCTTCGATCCCACTGTATGTACCTTACGTGCTGACAGCGCGGT 596
DB 360 ACTTCTGCTGCGCGCGCTTCGATCCCACTGTATGTACCTTACGTGCTGACAGCGCGGT 419
QY 597 GGAACCTCGCGCGCGCGCGCTGCTGCAAGCTGTGGTGGTAGTGAACCTGCTGTGCACT 656
DB 420 GGAACCTCGCGCGCGCGCGCGCTGCTGCAAGCTGTGGTGGTAGTGAACCTGCTGTGCACT 479
QY 657 CCTGCGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCGTGCGGTCAACCGAGCG 716
DB 480 CCTGCGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCGTGCGGTCAACCGAGCG 539
QY 717 TCTCATACCGGGGCCAGAGGGGTGACACGCGCGCGCGCACTGGGAGAAAGTCTGTGTGT 776
DB 540 TCTCATACCGGGGCCAGAGGGGTGACACGCGCGCGCGCACTGGGAGAAAGTCTGTGTGT 599
QY 777 GGGTCTGAGCTTCTGCTGTACGAGACAGCACTGAGCTGGAGTAGTACTGTCCGGGG 836
DB 600 GGGTCTGAGCTTCTGCTGTACGAGACAGCACTGAGCTGGAGTAGTACTGTCCGGGG 659
QY 837 GCAGCTCATCCCGAGGGGCACTGTATGCCAGTTCCTTCAAACTGTGTACTTCTCA 896
DB 660 GCAGCTCATCCCGAGGGGCACTGTATGCCAGTTCCTTCAAACTGTGTACTTCTCA 719
QY 897 TCAGGGCTTCCACCTCTGAGAGTTCTTACGCGCTTCTCAAGGTCACTTCTTAACTCA 956
DB 720 TCAGGGCTTCCACCTCTGAGAGTTCTTACGCGCTTCTTCAAGGTCACTTCTTAACTCA 779
QY 957 GCATCTACCTGAACATCCAGAGGGCGAACCGGCTCGGCTGAGTGGGGGCTCGAGAGGCGAG 1016
DB 780 GCATCTACCTGAACATCCAGAGGGCGAACCGGCTCGGCTGAGTGGGGGCTCGAGAGGCGAG 839

```

```

QY 1017 CCGGCGCGCGAGCCCTTCCTCCGAGGCGCCAGCCCTTCAACACCCCGCGCTGCTGTGG 1076
DB 840 GGGCGCGCGAGCCCTTCCTCCGAGGCGCCAGCCCTTCAACACCCCGCGCTGCTGTGG 899
QY 1077 GCTGCTGCGAGAAAGGGGCGACGGGGAGGCGCACTGCGCTGACAGGTATGGGGTGGGTGAG 1136
DB 900 GCTGCTGCGAGAAAGGGGCGACGGGGAGGCGCACTGCGCTGACAGGTATGGGGTGGGTGAG 959
QY 1137 CCGCGGTAGGCGCTGAGGCGCGGGGAGGCGACCTTCGGGGGTGGCGGTGGGGCGGCTCCG 1196
DB 960 CCGCGCGCGCGCGCTGAGGCTGGGGAGAGACAGCCCTCGGGGGTGGCGGTGGGGTGGCTCCG 1019
QY 1197 TGGCTTACACCACTTCAGACTTCGCGAGCTCTTCAGAGGGGCACTGAGAGCCGCGTCA 1256
DB 1020 CCGCTTACACCACTTCAGACTTCGCGAGCTCTTCAGAGGGGCACTGAGAGCCGCGTCA 1079
QY 1257 TCAGAGGGGCGTCCAGAGCGTGGGGTCTGCGCTTCGCTGGAGAAAGGCGCATGAGATGG 1316
DB 1080 TCAGAGGGGCGTCCAGAGCGTGGGGTCTGCGCTTCGCTGGAGAAAGGCGCATGAGATGG 1139
QY 1317 TGTCCAGAGCTTCAACCGAGCGCTTTCGCGTGTCTTCGCGGACAGAAAGTGGCAAGTCC 1376
DB 1140 TGTCCAGAGCTTCAACCGAGCGCTTTCGCGTGTCTTCGCGGACAGAAAGTGGCAAGTCC 1199
QY 1377 TGGCGCTCATGCTGAGCATCTTTGGGGCTGCTGCTGGGGCCCATACACGCTGCTGATGA 1436
DB 1200 TGGCGCTCATGCTGAGCATCTTTGGGGCTGCTGCTGGGGCCCATACACGCTGCTGATGA 1259
QY 1437 TCGGGGCGCGCGCGCATGAGCGCACTGCGTCCCGTCACTGATGAGAAACCTTCTTGCG 1496
DB 1260 TCGGGGCGCGCGCGCATGAGCGCACTGCGTCCCGTCACTGATGAGAAACCTTCTTGCG 1319
QY 1497 TCTGTGGGCGCAACTCGGCTGTCAACCTGTCTCTTACCTCTGTGCAACCAAGCTTCC 1556
DB 1320 TCTGTGGGCGCAACTCGGAGTCAACCTGTCTCTTACCTCTGTGCAACCAAGCTTCC 1379
QY 1557 GCGGGGCTTCAACCAAGCTGTCTGCGCGCGCGCAAGACTCAAAATCCAGCGCCCAAGTCC 1616
DB 1380 GCGGGGCTTCAACCAAGCTGTCTGCGCGCGCGCAAGACTCAAAATCCAGCGCCCAAGTCC 1439
QY 1617 TGGAGCACTGCTGGAAGTGAAGTGGCGCACAGAGCTCCCTGAGCGAGCGCTCTGACG 1676
DB 1440 TGGAGCACTGCTGGAAGTGAAGTGGCGCACAGAGCTCCCTGAGCGAGCGCTCTGACG 1499
QY 1677 CCAGGTCTCTGGGAGCATGAGCGCTGTGCGCCCTTACCCGAGCTGTTCCCGAGGGGTGA 1736
DB 1500 CCAGGTCTCTGGGAGCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1559
QY 1737 GCGCGCGCGGTGTCTGTGGCGCTCTCTTAAATGCGACGCGAGC 1777
DB 1560 GCGCGCGCGGTGTCTGTGGCGCTCTCTTAAATGCGACGCGAGC 1600

```

Search completed: June 2, 2005, 10:53:01  
 Job time : 11703.2 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 04:43:59 ; Search time 1440.49 Seconds  
(without alignments)  
11091.610 Million cell updates/sec

Title: US-10-727-021-5

Perfect score: 2699

Sequence: 1 ccacgcgcgcgcgcgtcga.....aaaaaaaaaaaaaaaaaaaaa 2699

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseqn1980s:\*  
2: geneseqn1980s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2699	100.0	2699	3	AAA09061 Human his
2	2699	100.0	2699	4	AAC62365 Complete
3	2699	100.0	2699	6	ABN84882 Human his
4	2699	100.0	2699	8	ABZ42533 Human his
5	2699	100.0	2699	9	ACC59394 Human his
6	2699	100.0	2699	10	ADD22860 Human ful
7	2699	100.0	2699	13	ADQ89179 Human tro
8	2699	100.0	2699	13	ADR31456 Human his
9	2635.2	97.6	2689	2	AAK02885 Human mac
10	2635.2	97.6	2689	2	AAK59167 Human G p
11	2635.2	97.6	2689	2	AAH44572 Human mus
12	2635.2	97.6	2689	8	ABX11852 Human cdn
13	2557.6	94.8	2576	5	AA876867 DNA encod
14	2149.2	79.6	2173	6	AA862391 cDNA sequ
15	1636.2	60.6	1902	4	AAK94219 Human ful
16	1636.2	60.6	1902	12	ADL30763 Full leng
17	1590.2	58.9	1893	3	AAK84582 G-protein
18	1590.2	58.9	1893	3	AAK70648 Human G-P
19	1397.8	51.8	1401	9	AA159976 Human wil
20	1384.8	51.3	3244	2	AAK59168 Rat G pro

21	1384.8	51.3	3244	2	AAH44574	AAH44574 Rat musca
22	1384.8	51.3	3244	8	ABX11853	ABX11853 Rat cDNA
23	1360.4	50.4	2050	8	AAK84572	AAK84572 Human G-P
24	1360.4	50.4	2050	3	AAK70637	AAK70637 Human G-P
25	1358.8	50.3	2761	10	ABT42301	ABT42301 Toxicity
26	1348.4	50.0	2483	12	ADO30256	ADO30256 Mouse GPC
27	1336.4	49.5	1335	12	ADO29966	ADO29966 Human GPC
28	1335	49.5	1335	3	AAK09062	AAK09062 Human his
29	1335	49.5	1335	4	AAC62366	AAC62366 cDNA enco
30	1335	49.5	1335	5	ACC59395	ACC59395 Human his
31	1335	49.5	1335	10	ADD22861	ADD22861 Human his
32	1335	49.5	1335	13	ADR31457	ADR31457 Human his
33	1331.8	49.3	1335	2	AAK02886	AAK02886 Human mac
34	1330.8	48.3	1334	2	AAH44573	AAH44573 Human mus
35	1303.8	48.3	1359	9	AA159978	AA159978 Human H3
36	1272.6	47.2	1293	9	AA159982	AA159982 Human H3
37	1208	44.8	2700	3	AAK70640	AAK70640 Rat G-pro
38	1207.8	44.7	1311	9	AA159979	AA159979 Human H3
39	1204.8	44.6	2700	2	AAK84571	AAK84571 G-protein
40	1201.8	44.5	1953	3	AAK70638	AAK70638 Rat G-pro
41	1178.6	43.7	1251	9	AA159983	AA159983 Human H3
42	1156	42.8	2145	5	AAK76868	AAK76868 DNA encod
43	1082.6	40.1	1203	9	AA159985	AA159985 Human H3
44	1075.2	39.8	18105	8	ABZ82337	ABZ82337 Mouse his
45	1072.2	39.7	1338	2	AAH44575	AAH44575 Rat musca

## ALIGNMENTS

RESULT 1  
AAA09061  
ID AAA09061 standard; cDNA; 2699 BP.  
AC AAA09061;  
DT 10-AUG-2000 (first entry)  
XX Human histamine H3 receptor cDNA.  
DE Human histamine H3 receptor; biogenic amine receptor homologue; ss.  
XX histamine H3 receptor; biogenic amine receptor homologue; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 299..1636  
FT /tag= a  
FT /product= "histamine\_H3\_receptor"  
XX  
XX WO200020011-A1.  
XX  
XX 13-APR-2000.  
XX  
XX 07-OCT-1998; 98WO-US021090.  
XX  
XX 07-OCT-1998; 98WO-US021090.  
XX  
XX (ORTH ) ORTHO-MCNELL PHARM INC.  
XX  
XX Lovenberg TW, Erlander M, Huvar A, Pyati J;  
XX WPI, 2000-303632/26.  
XX P-PSDB; AAY92218.  
XX  
XX Novel human histamine H3 receptor polynucleotides and polypeptides used  
XX in methods to identify modulators of receptor activity.  
XX  
XX Claim 2, Fig 1A-B; 54pp; English.  
XX  
XX The cDNA encodes the human histamine H3 receptor. The polypeptide  
XX contains the seven conserved hydrophobic domains and specific residues  
XX conserved in biogenic amine receptors. The human histamine H3 receptor  
XX polynucleotides and polypeptides are used in methods to screen for

modulators of receptor activity (claimed). Such agonists and antagonists may prove useful as research tools or may be used as therapeutics to treat disorders directly or indirectly involving histamine receptors (claimed). The characterization of the polynucleotide is useful for forensic analysis, diagnostic applications, and epidemiological studies

XX Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2699; DB 3; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 CCAACGGTCCCGCGGTGACAGGTGACCGGAGCGGCTCAGGCTCCGAGCTCTCTCC 60
DB 1 CCAACGGTCCCGCGGTGACAGGTGACCGGAGCGGCTCAGGCTCCGAGCTCTCTCC 60
QY 61 GCTGACAGCGCGGCTGCGGCGCCCACTGGGCTCCGATCCGAGCCCGGCTCTGGA 120
DB 61 GCTGACAGCGCGGCTGCGGCGCCCACTGGGCTCCGATCCGAGCCCGGCTCTGGA 120
QY 121 CCGGCTGCTCTGGGCGCGGCGCGGCGGAGCATGGGCTGGGCGCGCGGAGAA 180
DB 121 CCGGCTGCTCTGGGCGCGGCGCGGCGGAGCATGGGCTGGGCGCGCGGAGAA 180
QY 181 ACCCGACCCGCGCCAGAGGCGCCGAAAGAGAGGCTCCGAGCCGAGGCTCCGAGCG 240
DB 181 ACCCGACCCGCGCCAGAGGCGCCGAAAGAGAGGCTCCGAGCCGAGGCTCCGAGCG 240
QY 241 CCGAGCTCTGCGCGCGGCGGCTGCGGCGGCTCCGAGCGGAGGCTCTGCGGAGCA 300
DB 241 CCGAGCTCTGCGCGGCGGCTGCGGCGGCTCCGAGCGGAGGCTCTGCGGAGCA 300
QY 301 GGAGCGCGCGCGCGCGGCGGCGGCTGAGAGCTTGGGAGCGCTGAGCGGAGCA 360
DB 301 GGAGCGCGCGCGCGCGGCGGCGGCTGAGAGCTTGGGAGCGCTGAGCGGAGCA 360
QY 361 GGCGGCGGCGCGGCGGCGGCTTCTGCGAGCTGAGACCGGCGGCTGAGCGGCTCAT 420
DB 361 GGCGGCGGCGCGGCGGCGGCTTCTGCGAGCTGAGACCGGCGGCTGAGCGGCTCAT 420
QY 421 GGCGGCTGCTATGTTGGGCAAGGTGTTGGGCAAGCGGCTGATAGCTTGGCTTGGG 480
DB 421 GGCGGCTGCTATGTTGGGCAAGGTGTTGGGCAAGCGGCTGATAGCTTGGCTTGGG 480
QY 481 CCACTGAGGCTTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCGGCTCCGACTT 540
DB 481 CCACTGAGGCTTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCGGCTCCGACTT 540
QY 541 CCTGCTGCGGCGCTTCTGATCCACTGATATGACCTTACGTGAGCAAGCGGCTGAG 600
DB 541 CCTGCTGCGGCGCTTCTGATCCACTGATATGACCTTACGTGAGCAAGCGGCTGAG 600
QY 601 CTTTGGGCGGCGGCTTCTGCAAGTGTGGTGTGATGACCTTCTGCTGCACTCTCTC 660
DB 601 CTTTGGGCGGCGGCTTCTGCAAGTGTGGTGTGATGACCTTCTGCTGCACTCTCTC 660
QY 661 TGGCTTCAACATGATGCTCATGACGACGCTTCTGCTGAGTACCGGAGCGGCTCTC 720
DB 661 TGGCTTCAACATGATGCTCATGACGACGCTTCTGCTGAGTACCGGAGCGGCTCTC 720
QY 721 ATACCGGCGGCGGAGGAGTGAACGCGGCGGAGTGGGAGAGATGCTGCTGTTGGGT 780
DB 721 ATACCGGCGGCGGAGGAGTGAACGCGGCGGAGTGGGAGAGATGCTGCTGTTGGGT 780
QY 781 GCTGGGCTTCTGCTGTATGAGACCAAGCACTCTGAGCTGGAGTCTGCGGAGGAG 840
DB 781 GCTGGGCTTCTGCTGTATGAGACCAAGCACTCTGAGCTGGAGTCTGCGGAGGAG 840
QY 841 CTTCAATCCCGAGGAGGCACTGATGCGAGTTCCTTCAACTGATGTTCTTCACTAC 900
DB 841 CTTCAATCCCGAGGAGGCACTGATGCGAGTTCCTTCAACTGATGTTCTTCACTAC 900
QY 901 GGCTTCAACCTGAGATTCTTTAAGCCCTTCTCAAGCTCACTTCTTTAAGCTAGCAT 960
```

```
DB 901 GGCTTCAACCTGAGATTCTTTAAGCCCTTCTCAAGCTCACTTCTTTAAGCTAGCAT 960
QY 961 CTAACCTGAATCCAGAGGCGGACCGGCTCCGAGTGGAGGCTCGAGAGGAGCGG 1020
DB 961 CTAACCTGAATCCAGAGGCGGACCGGCTCCGAGTGGAGGCTCGAGAGGAGCGG 1020
QY 1021 CCGGAGCGGCTCCGAGGCGGAGGCTCAGCAGCCGAGCGGCTGCTGAGGCTG 1080
DB 1021 CCGGAGCGGCTCCGAGGCGGAGGCTCAGCAGCCGAGCGGCTGCTGAGGCTG 1080
QY 1081 CTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 CTGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 CGTAGGCGGTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 CGTAGGCGGTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 TTACCCACCTCAGGCTCCGAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1260
DB 1201 TTACCCACCTCAGGCTCCGAGGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 1260
QY 1261 GAGGAGGCTCAAGCGGCTGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
DB 1261 GAGGAGGCTCAAGCGGCTGAGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1320
QY 1321 CAGAGCTTCAACCGGCTTCCGAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1380
DB 1321 CAGAGCTTCAACCGGCTTCCGAGTGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 1380
QY 1381 CGTCACTGAGACATCTTGGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
DB 1381 CGTCACTGAGACATCTTGGGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1440
QY 1441 GGCGGCTGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
DB 1441 GGCGGCTGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1500
QY 1501 GTGGGCAACTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
DB 1501 GTGGGCAACTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560
QY 1561 GGCGCTTCAACCAAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
DB 1561 GGCGCTTCAACCAAGGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1620
QY 1621 GCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
DB 1621 GCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1680
QY 1681 GTCTCTGGGCACTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
DB 1681 GTCTCTGGGCACTGGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1740
QY 1741 GCGCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
DB 1741 GCGCGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
QY 1801 CTGGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
DB 1801 CTGGGTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1860
QY 1861 CCAATTTGGGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
DB 1861 CCAATTTGGGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1920
QY 1921 CTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
DB 1921 CTTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1980
QY 1981 GTGTCTCAGGCTTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2040
```





QY 721 ATACGGGGCCAGACAGGGTGAACCGGGGGGGAGTGGGAAAGATGCTGTGTGGGT 780  
Db 721 ATACGGGGCCAGACAGGGTGAACCGGGGGGGAGTGGGAAAGATGCTGTGTGGGT 780  
QY 781 GGTGGGCTTCTGCTGTACGAGACAGCCATCTGAGACTGGGAGTACTGTCCGGGGGGCAG 840  
Db 781 GGTGGGCTTCTGCTGTACGAGACAGCCATCTGAGACTGGGAGTACTGTCCGGGGGGCAG 840  
QY 841 CTCATCCCCGAGGGGCACTGCTATGCGAGTTCCTCTCAACTGTGTACTTCTCTCATAC 900  
Db 841 CTCATCCCCGAGGGGCACTGCTATGCGAGTTCCTCTCAACTGTGTACTTCTCTCATAC 900  
QY 901 GGGCTTCCACCTGAGAGTCTTTACGCGCTTCTCTCAGCGTCACTCTTTTAACTCAGCAT 960  
Db 901 GGGCTTCCACCTGAGAGTCTTTACGCGCTTCTCTCAGCGTCACTCTTTTAACTCAGCAT 960  
QY 961 CTACCTGAACATTCAGAGGGGCAACCGGCTTCGGGCTGTGATGGGGGCTCCAGAGGACGCGG 1020  
Db 961 CTACCTGAACATTCAGAGGGGCAACCGGCTTCGGGCTGTGATGGGGGCTCCAGAGGACGCGG 1020  
QY 1021 CCCCCGACCCCTCCGAGAGCCAGGCGCTCACCAACCCGACGCGCTGCTGCTGGGGCTG 1080  
Db 1021 CCCCCGACCCCTCCGAGAGCCAGGCGCTCACCAACCCGACGCGCTGCTGCTGGGGCTG 1080  
QY 1081 CTGGGAGAAAGGGGCAAGGGAGGCGCATGCGCTGCAAGGTATGGGGTGGGTGAGGCGGC 1140  
Db 1081 CTGGGAGAAAGGGGCAAGGGAGGCGCATGCGCTGCAAGGTATGGGGTGGGTGAGGCGGC 1140  
QY 1141 CGTAGGCGCTGAGGCGGGGAGGCGCAACCTCGGGGGTGGCGGTGGGGGCGGCTCCGTGGC 1200  
Db 1141 CGTAGGCGCTGAGGCGGGGAGGCGCAACCTCGGGGGTGGCGGTGGGGGCGGCTCCGTGGC 1200  
QY 1201 TTCAACCCACCTCAGCTCCGAGAGCTCTGAGAGGGGCACTGAGAGGCGGCGCTCACTCA 1260  
Db 1201 TTCAACCCACCTCAGCTCCGAGAGCTCTGAGAGGGGCACTGAGAGGCGGCGCTCACTCA 1260  
QY 1261 GAGGGGCTTCAAGCGGTGCGCGCTCTGCGGCTCTGAGAGAAAGCGCATGAGATGGTGTG 1320  
Db 1261 GAGGGGCTTCAAGCGGTGCGCGCTCTGCGGCTCTGAGAGAAAGCGCATGAGATGGTGTG 1320  
QY 1321 CCAGAGCTTCAACCCAGCGCTTTCGGGTGTCTGGGAGAGAGAAAGTGGCCAAAGTGGTGGC 1380  
Db 1321 CCAGAGCTTCAACCCAGCGCTTTCGGGTGTCTGGGAGAGAGAAAGTGGCCAAAGTGGTGGC 1380  
QY 1381 CGTCACTGAGAGCATTTTGGGCTGTGCTGGGCGCCATACAGCTGCTGATGATCAATCCG 1440  
Db 1381 CGTCACTGAGAGCATTTTGGGCTGTGCTGGGCGCCATACAGCTGCTGATGATCAATCCG 1440  
QY 1441 GGGCGGCTGCAATGAGCACTGCGTCCGTGATCTGATGATGAAACCTCTTCTGAGCTCT 1500  
Db 1441 GGGCGGCTGCAATGAGCACTGCGTCCGTGATCTGATGATGAAACCTCTTCTGAGCTCT 1500  
QY 1501 GGGGGGCAATGGGCTGTCAACCTCTTACCCTCTGTGTCACCAAGCTTCCGCGG 1560  
Db 1501 GGGGGGCAATGGGCTGTCAACCTCTTACCCTCTGTGTCACCAAGCTTCCGCGG 1560  
QY 1561 GGGCTTCAACCAAGAGCTGTGCGGCGCCAGAAAGCTCAAAATCCAGGCCCAAGCTCTCTGAA 1620  
Db 1561 GGGCTTCAACCAAGAGCTGTGCGGCGCCAGAAAGCTCAAAATCCAGGCCCAAGCTCTCTGAA 1620  
QY 1621 GCACTGTGGAAGTGAAGTGGCCCAACCAAGAGCTCTCTCAGCCAGCGCTCTCAGGCCAG 1680  
Db 1621 GCACTGTGGAAGTGAAGTGGCCCAACCAAGAGCTCTCTCAGCCAGCGCTCTCAGGCCAG 1680  
QY 1681 GTTCTCTGGGCAATCTGAGCGCTGTGCGGCTTACCGGGCTGTCTCCCAAGGGGTGAGCCC 1740  
Db 1681 GTTCTCTGGGCAATCTGAGCGCTGTGCGGCTTACCGGGCTGTCTCCCAAGGGGTGAGCCC 1740  
QY 1741 GCGCGGTGTGAGGCGCTCTCTTAATGCAAGGAGGAGCAACCGGCAATGAGAGGCGCTTC 1800  
Db 1741 GCGCGGTGTGAGGCGCTCTCTTAATGCAAGGAGGAGCAACCGGCAATGAGAGGCGCTTC 1800  
QY 1801 CTGGGTTGGCCAGAGGGCCCTCACTGAGTGAAGTGAAGGCTGGGTGGCGGCGCTCTGCC 1860

Db 1801 CTGGGTTGGCCAGAGGGCCCTCACTGAGTGAAGTGAAGGCTGGGTGGCGGCGCTCTGCC 1860  
QY 1861 CCCAATTTCTGGCTCACCGGGGAGAGGACAGTCTGAAGTTCACAGATGCTGCCACCC 1920  
Db 1861 CCCAATTTCTGGCTCACCGGGGAGAGACAGTCTGAAGTTCACAGATGCTGCCACCC 1920  
QY 1921 CCTGTGTGAGCCACCTTTCAGTACTGTGTGTGTCTTCCCAAGACAGCACTGG 1980  
Db 1921 CCTGTGTGAGCCACCTTTCAGTACTGTGTGTGTGTCTTCCCAAGACAGCACTGG 1980  
QY 1981 GTGTGCTCCAGGCTTCTGCGCTTACGAGTTCCTCTGTGACGTGACACACTGCAACCC 2040  
Db 1981 GTGTGCTCCAGGCTTCTGCGCTTACGAGTTCCTCTGTGACGTGACACACTGCAACCC 2040  
QY 2041 CCGTGAACACCTGACACCGGCTCTCCCGGAGCAAGGCCAGGACCTGCTTGTGCTG 2100  
Db 2041 CCGTGAACACCTGACACCGGCTCTCCCGGAGCAAGGCCAGGACCTGCTTGTGCTG 2100  
QY 2101 CCTTCTGTCTCTGTGATTAAGCTCAGGCTGAGCCCTTTCACCCCTTCCCAACTCT 2160  
Db 2101 CCTTCTGTCTCTGTGATTAAGCTCAGGCTGAGCCCTTTCACCCCTTCCCAACTCT 2160  
QY 2161 CTGTGCGGCGGCAAGGTGCAAGGGGCGCTGAGAACCTGAGACTGTCTGTGCTTTTCCA 2220  
Db 2161 CTGTGCGGCGGCAAGGTGCAAGGGGCGCTGAGAACCTGAGACTGTCTGTGCTTTTCCA 2220  
QY 2221 TTCTGGGTCTTTTCAGAAAGATGAAGAAAGAAACATGCTGTGAACCTGATGTTGGTGG 2280  
Db 2221 TTCTGGGTCTTTTCAGAAAGATGAAGAAAGAAACATGCTGTGAACCTGATGTTGGTGG 2280  
QY 2281 ATGTTTAATCAAGAGAGACAAATATGCTGAGAGGCTCAGGGCTGAGATTGGCAGTGGG 2340  
Db 2281 ATGTTTAATCAAGAGAGACAAATATGCTGAGAGGCTCAGGGCTGAGATTGGCAGTGGG 2340  
QY 2341 CTGCCAGCGGCTCTTCCCTCGCTAAGGCTTCCGCTGAGCTGTGCCAGCTGCTTCTGCC 2400  
Db 2341 CTGCCAGCGGCTCTTCCCTCGCTAAGGCTTCCGCTGAGCTGTGCCAGCTGCTTCTGCC 2400  
QY 2401 CACCGCGGCTCTGGGCTCAACACAGCGCTGAGGCGCAAGCGCGCCGCGCACTGTGTT 2460  
Db 2401 CACCGCGGCTCTGGGCTCAACACAGCGCTGAGGCGCAAGCGCGCGCGCACTGTGTT 2460  
QY 2461 GCTCAACCAAGAGACCTCTGGGGGTGTGTGGAGAGAGGGGCGCGGCTGGGCGCAGAGGTCC 2520  
Db 2461 GCTCAACCAAGAGACCTCTGGGGGTGTGTGGAGAGAGGGGCGCGGCTGGGCGCAGAGGTCC 2520  
QY 2521 CAAGGCTGACAGGGGCGGTCCAGAGAGGTGCCGGGCAAGGGCGCTTCCCAATGTGCT 2580  
Db 2521 CAAGGCTGACAGGGGCGGTCCAGAGAGGTGCCGGGCAAGGGCGCTTCCCAATGTGCT 2580  
QY 2581 GTGACACCGGTGCAAGCGCTGTGACAGTCCCTGTGCTGTGCGGCTGCGGCGCTGCA 2640  
Db 2581 GTGACACCGGTGCAAGCGCTGTGACAGTCCCTGTGCTGTGCGGCTGCGGCGCTGCA 2640  
QY 2641 AACCGTGAAGTCAATTAAGTGTATTTTAAAAAAGTGTATTTTAAAAAAGTGTATTTTAAAAA 2699  
Db 2641 AACCGTGAAGTCAATTAAGTGTATTTTAAAAAAGTGTATTTTAAAAAAGTGTATTTTAAAAA 2699

RESULT 3  
ABN84882  
ID ABN84882 standard; cDNA; 2699 BP.  
XX ABN84882;  
AC  
XX  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human histamine H3 receptor cDNA.  
XX  
XX Histamine; receptor; G-protein coupled receptor; human; neuroprotective;  
KW carbidant; antidepressant; tranquilizer; antiparkinsonian; anorectic;  
KW hypotensive; analgesic; antidiabetic; laxative; antiarrhythmic; antituber;



Db 1321 CAGAGCTTACCCAGGCTTTCTGCTGCTGCGGACAGAAAGTGCCAAAGCTGCTGCG 1380  
Qy 1381 CCGTCAATCGAGACATTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATGATCATCCG 1440  
Db 1381 CCGTCAATCGAGACATTTTGGGCTCTGCTGGGCCCCATACAGCTGTGATGATCATCCG 1440  
Qy 1441 GGCCCGCTGCGCATGCGCATCTGCTGCTGATCTAGTGTGATCGAAACCTCTTCTGCTGCT 1500  
Db 1441 GGCCCGCTGCGCATGCGCATCTGCTGCTGATCTAGTGTGATCGAAACCTCTTCTGCTGCT 1500  
Qy 1501 GTGGGCGCAATGCGGCTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
Db 1501 GTGGGCGCAATGCGGCTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1560  
Qy 1561 GGCCCTTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
Db 1561 GGCCCTTACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620  
Qy 1621 GCACTGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680  
Db 1621 GCACTGCTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1680  
Qy 1681 GTCTCTGCGGCAATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
Db 1681 GTCTCTGCGGCAATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1740  
Qy 1741 CCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
Db 1741 CCGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1800  
Qy 1801 CTGGGTTGGCCAGAGGCGCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
Db 1801 CTGGGTTGGCCAGAGGCGCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1860  
Qy 1861 CCGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
Db 1861 CCGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
Qy 1921 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
Db 1921 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
Qy 1981 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
Db 1981 GTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
Qy 2041 CCGTGAACACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAAC 2100  
Db 2041 CCGTGAACACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAACCTGCAAC 2100  
Qy 2101 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
Db 2101 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
Qy 2161 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220  
Db 2161 CCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2220  
Qy 2221 TTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
Db 2221 TTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
Qy 2281 ATGTTTAATCAAGAGAGCAAAATGCTGAGAGCTGAGGCTGAGTTGGAGGTTGGG 2340  
Db 2281 ATGTTTAATCAAGAGAGCAAAATGCTGAGAGCTGAGGCTGAGTTGGAGGTTGGG 2340  
Qy 2341 CTGCCACGCGCTCTCTCCCTCGCTAAGAGGCTTCGCGCTGAGCTGTGCTGCTGCTGCT 2400  
Db 2341 CTGCCACGCGCTCTCTCCCTCGCTAAGAGGCTTCGCGCTGAGCTGTGCTGCTGCTGCT 2400  
Qy 2401 CACCCGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
Db 2401 CACCCGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460

Db 2401 CACCCGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2460  
Qy 2461 GCTCAACCAAGACCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520  
Db 2461 GCTCAACCAAGACCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2520  
Qy 2521 CAAGGCTGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
Db 2521 CAAGGCTGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2580  
Qy 2581 GTGCAACCGCTGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
Db 2581 GTGCAACCGCTGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640  
Qy 2641 AACCGTGAAGTGCACATTAAGTATTTTAAAAA 2699  
Db 2641 AACCGTGAAGTGCACATTAAGTATTTTAAAAA 2699  
RESULT 4  
AB242533  
ID AB242533 standard; DNA; 2699 BP.  
XX  
XX AB242533;  
AC  
XX  
XX 04-MAR-2003 (first entry)  
DT  
XX  
XX  
DE Human histamine H3 receptor nucleotide SEQ ID NO:548.  
XX  
XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor; modulator; antibody; immune-related disease;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related disease; cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW gastritis; host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer; gene; ds.  
XX  
XX Homo sapiens.  
OS  
XX WO200261087-A2.  
PN  
XX  
XX  
PD 08-AUG-2002.  
XX  
XX 19-DEC-2001; 2001MO-US050107.  
PF  
XX  
XX 19-DEC-2000; 2000US-0257144P.  
PR  
XX  
XX (LIFE-) LIFESPAN BIOSCIENCES INC.  
PA  
XX  
XX Burner GC, Roush CL, Brown JP;  
PI  
XX  
XX WPI; 2003-046718/04.  
DR P-PSDB; ABP81687.  
DR  
XX  
XX  
PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX  
XX  
PS Disclosure; Fig 1; 523pp; English.  
XX  
XX The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific

antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for GPCRs and antibodies are useful for diagnosing and designing drugs for treating immune-related diseases, growth-related diseases, cell regeneration-related diseases, immunological-related cell proliferative diseases, or auto-immune diseases, e.g. AIDS, Alzheimer's disease, atherosclerosis, bacterial, fungal, protozoan or viral infections, osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute inflammation, allergies, Crohn's disease, diabetes, graft versus host disease, Parkinson's disease, multiple sclerosis, pain, psoriasis, anxiety, depression, schizophrenia, dementia, mental retardation, memory loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or any other disorder in which GPCRs are involved. The antibodies may be used in immunoassays and immunodiagnosis. AB242523 to AB24869 encode GPCR proteins given in ABP81675 to ABP82018, which are used in the exemplification of the present invention

Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2699; DB 8; Length 2699;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;

Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACGCGTCCGCGGCTGCAAGTCCGACCGGACGCGCTCAGAGCTCCGCTCTCTCC 60  
 DB 1 CCACGCGTCCGCGGCTGCAAGTCCGACCGGACGCGCTCAGAGCTCCGCTCTCTCC 60  
 QY 61 GCTGAGACGCGCGGCTGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
 DB 61 GCTGAGACGCGCGGCTGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120  
 QY 121 CCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 180  
 DB 121 CCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 180  
 QY 181 ACCGACCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 240  
 DB 181 ACCGACCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 240  
 QY 241 CCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 300  
 DB 241 CCGGCTGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 300  
 QY 301 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 360  
 DB 301 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 360  
 QY 361 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 420  
 DB 361 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 420  
 QY 421 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 480  
 DB 421 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 480  
 QY 481 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 540  
 DB 481 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 540  
 QY 541 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 600  
 DB 541 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 600  
 QY 601 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 660  
 DB 601 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 660  
 QY 661 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 720  
 DB 661 GGAAGCGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 720  
 QY 721 ATACGCGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 780

DB 721 ATACGCGGCGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 780  
 QY 781 GCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 840  
 DB 781 GCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 840  
 QY 841 CTCATCCCGGAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 900  
 DB 841 CTCATCCCGGAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 900  
 QY 901 GGGTTCACCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 960  
 DB 901 GGGTTCACCGGAGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 960  
 QY 961 CTCATCCCGGAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 1020  
 DB 961 CTCATCCCGGAGGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 1020  
 QY 1021 CCGGAGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 1080  
 DB 1021 CCGGAGCGGCTTCCGAGGCGGCTTCCGAGGCGGCTTCCGAGGCGGCTTCCGAGGCGGCT 1080  
 QY 1081 CTGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGG 1140  
 DB 1081 CTGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGG 1140  
 QY 1141 CTTAGGCGGCTGAGGCGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGG 1200  
 DB 1141 CTTAGGCGGCTGAGGCGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGGCAAGGCGG 1200  
 QY 1201 TTACACCACTCCAGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1260  
 DB 1201 TTACACCACTCCAGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1260  
 QY 1261 GAGGCGGCTCCAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1320  
 DB 1261 GAGGCGGCTCCAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1320  
 QY 1321 CCAAGCTTCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1380  
 DB 1321 CCAAGCTTCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1380  
 QY 1381 CCAAGCTTCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1440  
 DB 1381 CCAAGCTTCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1440  
 QY 1441 GGGCGGCTGCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1500  
 DB 1441 GGGCGGCTGCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1500  
 QY 1501 GGGCGGCTGCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1560  
 DB 1501 GGGCGGCTGCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1560  
 QY 1561 GGGCGGCTGCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1620  
 DB 1561 GGGCGGCTGCAAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1620  
 QY 1621 GCACTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1680  
 DB 1621 GCACTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1680  
 QY 1681 GCTCTCTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1740  
 DB 1681 GCTCTCTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1740  
 QY 1741 CCGCGGCTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1800  
 DB 1741 CCGCGGCTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1800  
 QY 1801 CCGCGGCTGCGGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCTCCGAGGCGGCT 1860

```

Db 1801 CTGGGTTGGCCAGAGGAGCCCTCACTGCTGCACTGAGAGCTGAGTGGCCGCGCCCTGCC 1860
Qy 1861 CCCACATTCGTGGCTCCACCGGGGAGGAGACGTCTGAGAGTCCAGACATGCTGCCACCC 1920
Db 1861 CCCACATTCGTGGCTCCACCGGGGAGGAGACGTCTGAGAGTCCAGACATGCTGCCACCC 1920
Qy 1921 CCTGCTGTTGCTCCACCGCTTCCAGATTACTGTTGTTGTTCTTCCAAAGCAAGACCTG 1980
Db 1921 CCTGCTGTTGCTCCACCGCTTCCAGATTACTGTTGTTGTTCTTCCAAAGCAAGACCTG 1980
Qy 1981 GTGTGCTCAGAGCTTCCCTGAGAGCTTTCGAGAGCTTTCGAGAGCTTTCGAGAGCTT 2040
Db 1981 GTGTGCTCAGAGCTTCCCTGAGAGCTTTCGAGAGCTTTCGAGAGCTTTCGAGAGCTT 2040
Qy 2041 CCTGACACACCTGACACCTGACCTGCTCCCTCCGAGCAAGCCAGACACCTGCTTGTG 2100
Db 2041 CCTGACACACCTGACACCTGACCTGCTCCCTCCGAGCAAGCCAGACACCTGCTTGTG 2100
Qy 2101 CCTTCTGCTCTTTCGATTAAGCTCAGGCTGAGCTTTCACCCCTTCCCAACACTCT 2160
Db 2101 CCTTCTGCTCTTTCGATTAAGCTCAGGCTGAGCTTTCACCCCTTCCCAACACTCT 2160
Qy 2161 CTCTGCCCCCAAAAGTGTCAAGAGGCTTGAAGAACTCGAAGCTTCTCTGCTTTTCA 2220
Db 2161 CTCTGCCCCCAAAAGTGTCAAGAGGCTTGAAGAACTCGAAGCTTCTCTGCTTTTCA 2220
Qy 2221 TTCTGGGTTGTTTCAAGAAAGTGAAGAGAAACATGCTGAGAACTTGAAGTTGCTGG 2280
Db 2221 TTCTGGGTTGTTTCAAGAAAGTGAAGAGAAACATGCTGAGAACTTGAAGTTGCTGG 2280
Qy 2281 ATGTTTAAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGCTGAGATTGAGAGTGG 2340
Db 2281 ATGTTTAAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGCTGAGATTGAGAGTGG 2340
Qy 2341 CTCCACGCGCTCTCTCCCTCCCTGAGAGCTTCCGCTGAGAGCTTTCGAGAGCTTTC 2400
Db 2341 CTCCACGCGCTCTCTCCCTCCCTGAGAGCTTCCGCTGAGAGCTTTCGAGAGCTTTC 2400
Qy 2401 CACCCGCTCTGAGGCTCAGACAGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 2460
Db 2401 CACCCGCTCTGAGGCTCAGACAGGCTGAGAGCTGAGAGCTGAGAGCTGAGAGCTG 2460
Qy 2461 GGTCAACCCAGAGACCTTGGGGGTTGTTGAGAGAGAGGAGGCGCGCTGAGAGGCTC 2520
Db 2461 GGTCAACCCAGAGACCTTGGGGGTTGTTGAGAGAGAGGAGGCGCGCTGAGAGGCTC 2520
Qy 2521 CAAAGGCTCAGAGGCGGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
Db 2521 CAAAGGCTCAGAGGCGGCTCAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2580
Qy 2581 GTGACACCGTGCACGCGCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Db 2581 GTGACACCGTGCACGCGCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2640
Qy 2641 AACCGTAGGTCACAATAAAGTGTATTTTAAAAA 2699
Db 2641 AACCGTAGGTCACAATAAAGTGTATTTTAAAAA 2699

```

RESULT 5  
ACCS9394  
ID ACCS9394 standard; DNA; 2699 BP.

ACCS9394;

28-AUG-2003 (first entry)

Human histamine H3 receptor nucleotide sequence.

Human histamine H3 receptor; gene; ds; agonist;  
nocotropic; neuroprotective; cerebroprotective; cardiant; antidiabetic;  
immunomodulatory; gastrointestinal; antiallergic; antidiabetic;  
antiinflammatory; hypotensive; antiarrhythmic.

```

XX Homo sapiens.
OS
XX
XX MO2003044059-A1.
PN
XX
XX 30-MAY-2003.
PD
XX
XX 15-NOV-2001; 2001WO-US045313.
PF
XX
XX 15-NOV-2001; 2001WO-US045313.
PR
XX
XX (ORTH ) ORTHO-MCNEIL PHARM INC.
PA
XX
XX Lovenberg T;
PI
XX
XX MPI; 2003-457595/43.
DR
XX
XX
XX Identifying agonists of recombinant human histamine H3 receptor protein
PT activity, useful for diagnosing and treating H3 receptor-related
PT disorders, such as nervous system disorders, asthma, allergy,
PT hypertension and diabetes.
PT
XX
XX
XX Example 1; Fig 1; 55pp; English.
PS
XX
XX The present invention relates to a method of identifying compounds that
CC are agonists of recombinant human histamine H3 receptor protein activity,
CC comprising combining a compound suspected of being an antagonist of human
CC histamine H3 receptor protein activity with recombinant human histamine
CC H3 receptor protein, and measuring an agonistic effect of the compound on
CC the recombinant human histamine H3 receptor protein. The methods and
CC compositions of the present invention are useful for diagnosing and
CC treating human histamine H3 receptor-related disorders, such as central
CC and peripheral nervous system disorders (depression, anxiety, psychosis,
CC Parkinson's disease, Alzheimer's disease, dementia and tardive
CC dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune,
CC cardiovascular (hypertension, and arrhythmia) and gastrointestinal
CC disorders. The present sequence is the coding sequence of the human
CC histamine H3 receptor
CC
XX
XX Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;
SQ

```

Query Match 100.0%; Score 2699; DB 9; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 CCAAGCGTCCGCGCTGAGAGTGCACCGGAGCGGCTGAGGCTGCTCTCC 60
Db 1 CCAAGCGTCCGCGCTGAGAGTGCACCGGAGCGGCTGAGGCTGCTCTCC 60
Qy 61 GTGACAGAGCGCGCTGCGGCTCCCACTGAGCTGAGTCCGAGCCCGCTCGCA 120
Db 61 GTGACAGAGCGCGCTGCGGCTCCCACTGAGCTGAGTCCGAGCCCGCTCGCA 120
Qy 121 CCGCTGCTTGGCCCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 180
Db 121 CCGCTGCTTGGCCCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGCGGCGG 180
Qy 181 ACCCGACCGGCGCAAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Db 181 ACCCGACCGGCGCAAGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 241 CCAAGCTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Db 241 CCAAGCTCTGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Qy 301 GAGGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Db 301 GAGGCGCGGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
Qy 361 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 361 GCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420

```

QY	421	GGCGCTGCTCATCGTGGGCAAGGTGCTGGGCAAGCGCTGGTCATGCTCGCTTGTTGGG	480
Dp	421	GGCGCTGCTCATCGTGGGCAAGGTGCTGGGCAAGCGCTGGTCATGCTCGCTTGTTGGG	480
QY	481	CGACTCGAGCGCTCGGCAACCAATTCTTCTCGTCAACCTCGGCACTTCGCACTT	540
Dp	481	CGACTCGAGCGCTCGGCAACCAATTCTTCTCGTCAACCTCGGCACTTCGCACTT	540
QY	541	CCTGCTCGAGCGCTTTCGATCCCACTATATGACCTTACGTGTGACAGGCGCGTGGAC	600
Dp	541	CCTGCTCGAGCGCTTTCGATCCCACTATATGACCTTACGTGTGACAGGCGCGTGGAC	600
QY	601	CTTGCGGCGGAGCGCTTTCGAGACTGTGGCTGGTAGTGACTACCTGTGTGCACCTCTCTC	660
Dp	601	CTTGCGGCGGAGCGCTTTCGAGACTGTGGCTGGTAGTGACTACCTGTGTGCACCTCTCTC	660
QY	661	TGCGCTTCAACATTCGTGCTCATCAGTACGCGCTTCTGTGCGGACCGAGCGGTCTC	720
Dp	661	TGCGCTTCAACATTCGTGCTCATCAGTACGCGCTTCTGTGCGGACCGAGCGGTCTC	720
QY	721	ATACCGGGCGCAGAGGAGGTGACACGCGGCGGGCAGTGGGAAAGATGTGCTGTGTGGGT	780
Dp	721	ATACCGGGCGCAGAGGAGGTGACACGCGGCGGGCAGTGGGAAAGATGTGCTGTGTGGGT	780
QY	781	GCTGGCGCTTCTGTGTGACGGAACAGCAGCATCTGTAGCTGGAGATACCTGTGCGGGGAG	840
Dp	781	GCTGGCGCTTCTGTGTGACGGAACAGCAGCATCTGTAGCTGGAGATACCTGTGCGGGGAG	840
QY	841	CTCCATCCCGGAGGGGCACTGCTATGCGGAGATTTCTTACAACTGGTACTTCTCATAC	900
Dp	841	CTCCATCCCGGAGGGGCACTGCTATGCGGAGATTTCTTACAACTGGTACTTCTCATAC	900
QY	901	GGCTTTCACCTGAGAGTCTTTTACGCGCTTCTCTCAGCGTCACTCTTTAACCCTCAGCAT	960
Dp	901	GGCTTTCACCTGAGAGTCTTTTACGCGCTTCTCTCAGCGTCACTCTTTAACCCTCAGCAT	960
QY	961	CTACTCTGAATCCAGAGGCGCACCCGCGCTCGGCTGGATGGGGCTCGAGAGGACGCGG	1020
Dp	961	CTACTCTGAATCCAGAGGCGCACCCGCGCTCGGCTGGATGGGGCTCGAGAGGACGCGG	1020
QY	1021	CCCCGAGCGCCCTTCCGAGGCGCCAGCGCTCACCAACCCGCTGGCTGCTGGGGCTG	1080
Dp	1021	CCCCGAGCGCCCTTCCGAGGCGCCAGCGCTCACCAACCCGCTGGCTGCTGGGGCTG	1080
QY	1081	CTGGGAGAAAGGGGACGCGGGAGGGCACTGCGCTGACAGGATATGGGGGTGGTGAAGCGCG	1140
Dp	1081	CTGGGAGAAAGGGGACGCGGGAGGGCACTGCGCTGACAGGATATGGGGGTGGTGAAGCGCG	1140
QY	1141	CGTAGGCGCTTAGGCGCGGGAGGAGCGACCTCGGGGGTGGCGATGGGCGCGCTCCGTGGC	1200
Dp	1141	CGTAGGCGCTTAGGCGCGGGAGGAGCGACCTCGGGGGTGGCGATGGGCGCGCTCCGTGGC	1200
QY	1201	TTCAACCACTTCAGCTTCGCGAGCTCTTCGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
Dp	1201	TTCAACCACTTCAGCTTCGCGAGCTCTTCGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
QY	1261	GAGGGGCGCTCCAAAGCGCTGCGGCTCTCGGCGCTCGTGAAGAAAGCGCAAGAAATGTGTCTC	1320
Dp	1261	GAGGGGCGCTCCAAAGCGCTGCGGCTCTCGGCGCTCGTGAAGAAAGCGCAAGAAATGTGTCTC	1320
QY	1321	CCAGAGCTTACCAAGCGCTTTCGCGCTTTCGCGGACAGAAAGTGGCCAAGTGCCTGC	1380
Dp	1321	CCAGAGCTTACCAAGCGCTTTCGCGCTTTCGCGGACAGAAAGTGGCCAAGTGCCTGC	1380
QY	1381	CGTCATCGTAGCATCTTTGGGCTCTGTGCTGGGCGCCCATACAGCGTGTGATGATCATCG	1440
Dp	1381	CGTCATCGTAGCATCTTTGGGCTCTGTGCTGGGCGCCCATACAGCGTGTGATGATCATCG	1440
QY	1441	GGCGGCGCGCATGGGCACTGCGTCCCGAATACTGGTAGAAGAAACCTCTCTTGGGCTCT	1500
Dp	1441	GGCGGCGCGCATGGGCACTGCGTCCCGAATACTGGTAGAAGAAACCTCTCTTGGGCTCT	1500
QY	1501	GTTGGGCCAATCGGCTGTCAACCCGTGCTCTTCACTCTTGTGGCAACCAAGCTTTCGCGG	1560

Dp	1501	GTGGGGCAACCTGGCTGCAACCCCTGCTCTTACCCCTCTGTGCCACCAACACTTCCGCCG	1560
Qy	1561	GGCCCTTACCAAGCTGCTGTGCCCCCAGAAAGCTCAAAATCCAGGCCCAACAGCTCCCTGGA	1620
Dp	1561	GGCTTACCAAGCTGCTGTGCCCCCAGAAAGCTCAAAATCCAGGCCCAACAGCTCCCTGGA	1620
Qy	1621	GCACTGTGGAAGTGAAGTGGCCCAACAGAGCTCCCTCAGCCAGCCCTCTCTGACCCAG	1680
Dp	1621	GCACTGTGGAAGTGAAGTGGCCCAACAGAGCTCCCTCAGCCAGCCCTCTCTGACCCAG	1680
Qy	1681	GTCTCTGTGGGCACTGTGAGCCCTGTGCCCCCTTACCCCGCTGTTCCCCAGGGGATGAAGCC	1740
Dp	1681	GTCTCTGTGGGCACTGTGAGCCCTGTGCCCCCTTACCCCGCTGTTCCCCAGGGGATGAAGCC	1740
Qy	1741	CGCGGTGTCTGTGGGCCCTCTTATATGCAAGGAGGCAACCTGTGCATGTGAAGGCGCTTC	1800
Dp	1741	CGCGGTGTCTGTGGGCCCTCTTATATGCAAGGAGGCAACCTGTGCATGTGAAGGCGCTTC	1800
Qy	1801	CTGGGTTTGGCCAGAGGGGCCCTCACTGTGCTTGAATGAGGCTGTGGGTGGCCGGCCCTGCC	1860
Dp	1801	CTGGGTTTGGCCAGAGGGGCCCTCACTGTGCTTGAATGAGGCTGTGGGTGGCCGGCCCTGCC	1860
Qy	1861	CCCACTTCTGGCTCCACCGGGGAGGGACAGCTGTGAAGTCCAGACATGTCTGCCACCC	1920
Dp	1861	CCCACTTCTGGCTCCACCGGGGAGGGACAGCTGTGAAGTCCAGACATGTCTGCCACCC	1920
Qy	1921	CGTGCTGTGGCCCAACCCCTGTGCAGTTTACGTGTGGTGTCTTCCAAAGCAAGAACCTGG	1980
Dp	1921	CGTGCTGTGGCCCAACCCCTGTGCAGTTTACGTGTGGTGTCTTCCAAAGCAAGAACCTGG	1980
Qy	1981	GTGTGCTTCAGAGCTTCTGACCCTTACAGTTTGTCTGTGCAGTGCACACTGTCAACCC	2040
Dp	1981	GTGTGCTTCAGAGCTTCTGACCCTTACAGTTTGTCTGTGCAGTGCACACTGTCAACCC	2040
Qy	2041	CTGTGACACACTGTGCACACGCTCCCTTCCCCGGAACAAGCCAGAGACACTGCTTTGCTG	2100
Dp	2041	CTGTGACACACTGTGCACACGCTCCCTTCCCCGGAACAAGCCAGAGACACTGCTTTGCTG	2100
Qy	2101	CCTTCTGTCTTTCATTAAGGCTCAAGGCTGTGGCCCTTCAACCCCTTTCACCAACACTCT	2160
Dp	2101	CCTTCTGTCTTTCATTAAGGCTCAAGGCTGTGGCCCTTTCACCCCTTTCACCAACACTCT	2160
Qy	2161	CTGTGCCCCCAAAAGTGTCAAGGGGCCCCCTAGGAAGCTTCGAAAGCTTCTGTCTTTTCCA	2220
Dp	2161	CTGTGCCCCCAAAAGTGTCAAGGGGCCCCCTAGGAAGCTTCGAAAGCTTCTGTCTTTTCCA	2220
Qy	2221	TTCTGGGTGTTTTCAGAAAGATGAAGAGAAACATGTCTGTGAATTGATGTTCGTGGG	2280
Dp	2221	TTCTGGGTGTTTTCAGAAAGATGAAGAGAAACATGTCTGTGAATTGATGTTCGTGGG	2280
Qy	2281	ATGTTTATATCAAGAGACAAAATTGCTGAAGAGCTCAAGGCTTGAATTTGGCAGGTGTGGG	2340
Dp	2281	ATGTTTATATCAAGAGAGCAAAATTGCTGAAGAGCTCAAGGCTTGAATTTGGCAGGTGTGGG	2340
Qy	2341	CTCCACGAGCCCTCCCTCCGCTCAAGGCTTCGAGCTGTGTCAGAGCTGCTTCTGACC	2400
Dp	2341	CTCCACGAGCCCTCCCTCCGCTCAAGGCTTCGAGCTGTGTCAGAGCTGCTTCTGACC	2400
Qy	2401	CACCCCGGCTCTGGGCTTCAACAAGCCCTGTGTGCAAGGCTGCCCCGGCCACTCTGTTT	2460
Dp	2401	CACCCCGGCTCTGGGCTTCAACAAGCCCTGTGTGCAAGGCTGCCCCGGCCACTCTGTTT	2460
Qy	2461	GCTCAACCCAGGACCTCTGTGGGGGTTGTTGGAGAGAGGGGGCCCCGGCTGGGCCCAAGGTTCC	2520
Dp	2461	GCTCAACCCAGGACCTCTGTGGGGGTTGTTGGAGAGAGGGGGCCCCGGCTGGGCCCAAGGTTCC	2520
Qy	2521	CAAGGCGTGCAGGGGCGGTTCAGAGAGAGTGTCCCGGCGCAGGGGCGGCTTCGCCATGTGCT	2580
Dp	2521	CAAGGCGTGCAGGGGCGGTTCAGAGAGAGTGTCCCGGCGCAGGGGCGGCTTCGCCATGTGCT	2580
Qy	2581	GTGACCCGTGCAACGCGCTCTGTGACTCTCTTGCCTGTGCCCGGCTGTGCGCTGTGCTCA	2640

DB 2581 GTGACACCGCTGCAGCGCTCTGCATGCTCTGCTGTGCTGCCGCTGCGCTGCGCTGCA 2640  
QY 2641 AACCGTAGAGTCACATTAAGTATTTTAAAAA 2699  
DB 2641 AACCGTAGAGTCACATTAAGTATTTTAAAAA 2699  
RESULT 6  
ADD22860  
ID ADD22860 standard; cDNA; 2699 BP.  
XX ADD22860;  
AC ADD22860;  
XX 15-JAN-2004 (first entry)  
XX  
XX  
DE Human full length cDNA encoding histamine H3 receptor.  
XX  
XX Human; ss; Histamine H3 receptor; GPCR; G protein-coupled receptor; gene;  
XX depression; anxiety; schizophrenia; Parkinson's disease; obesity;  
XX hypertension; Tourette's syndrome; sexual dysfunction; drug addiction;  
XX drug abuse; cognitive disorder; Alzheimer's disease;  
XX obsessive-compulsive behaviour; panic attack; pain; eating disorder;  
XX anorexia; cardiovascular disorder; cerebrovascular disorder; diabetes;  
XX constipation; arrhythmia; ulcer; asthma; allergy; inflammation;  
XX prostate dysfunction.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 299..1636  
FT /tag= a  
FT /product= "Histamine H3 receptor"  
PN US6437100-B1.  
XX  
XX 20-ANG-2002.  
XX  
XX 21-ANG-2000; 2000US-00642514.  
XX  
XX 07-OCT-1998; 98US-00167354.  
XX  
XX (ORTH ) ORTHO PHARM CORP.  
XX  
XX Lovenberg TW, Erlander M, Huvar A, Pyati J;  
PI P-PSDB; ADD22854.  
XX  
XX WPI: 2003-810293/76.  
XX  
XX  
XX New antibody against human histamine H3 receptor, preferably with  
PT receptor antagonist activity, useful for diagnostic purposes and for  
PT treating diseases such as depression, Parkinson's disease, obesity or  
PT hypertension.  
XX  
XX Example 1; SEQ ID NO 5; 25bp; English.  
XX  
XX The invention relates to a monospecific antibody immunologically reactive  
CC with a protein appearing as ADD22854, where the protein functions as a  
CC human histamine H3 receptor. The antibody blocks intracellular signaling  
CC activity of the human histamine H3 receptor in response to ligand  
CC binding. The antibody is useful for detecting and quantifying expression  
CC of human histamine H3 receptors, which may be useful for diagnostic,  
CC epidemiological or forensic purposes. The antibody is potentially useful  
CC in treating diseases such as depression, anxiety, schizophrenia,  
CC Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual  
CC dysfunction, drug addiction or drug abuse, cognitive disorders, sexual  
CC Alzheimer's disease, obsessive-compulsive behaviour, panic attacks, pain,  
CC eating disorders and anorexia, cardiovascular and cerebrovascular  
CC disorders, diabetes, constipation, arrhythmia, ulcers, asthma, allergy,  
CC inflammation, or prostate dysfunction. The present sequence is the full  
CC length cDNA encoding the histamine H3 receptor.  
XX  
XX Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match 100.0%; Score 2699; DB 10; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCACGCTCCGCGGTGACACCGGAGGCTGAGGCTCCGCGCTCTCC 60  
DB 1 CCACGCTCCGCGGTGACACCGGAGGCTGAGGCTCCGCGCTCTCC 60  
QY 61 GCTGACAGACCGCGGTGACACCGGAGGCTGAGGCTCCGCGCTCTCC 120  
DB 61 GCTGACAGACCGCGGTGACACCGGAGGCTGAGGCTCCGCGCTCTCC 120  
QY 121 CCGCTGCTCTGAGCCCGGCGCCCGGCGGAGGCTGAGGCTCCGCGCTCTCC 180  
DB 121 CCGCTGCTCTGAGCCCGGCGCCCGGCGGAGGCTGAGGCTCCGCGCTCTCC 180  
QY 181 ACCCGACCGGCGGAGGCGGAGGCTGAGGCTCCGCGGCGGCGGCGGCGG 240  
DB 181 ACCCGACCGGCGGAGGCGGAGGCTGAGGCTCCGCGGCGGCGGCGGCGG 240  
QY 241 CCGAGCTCTGAGCCCGGCGGCGGCGGCGGAGGCTGAGGCTCCGCGGCGG 300  
DB 241 CCGAGCTCTGAGCCCGGCGGCGGCGGCGGAGGCTGAGGCTCCGCGGCGG 300  
QY 301 GGAAGCG 360  
DB 301 GGAAGCG 360  
QY 361 GCG 420  
DB 361 GCG 420  
QY 421 GCGCGCTGCTCATGTCGAGCGAGGCTGTCGAGCGGCTGTCATGCTGCTG 480  
DB 421 GCGCGCTGCTCATGTCGAGCGAGGCTGTCGAGCGGCTGTCATGCTGCTG 480  
QY 481 CGAATGAGCTCTCGGACCCGAGAACCACTTCTTCTGTCGAACTTCGACCTT 540  
DB 481 CGAATGAGCTCTCGGACCCGAGAACCACTTCTTCTGTCGAACTTCGACCTT 540  
QY 541 CCGTCGCGCGCGCTTCTGATCCCACTGATGATGATGATGATGATGATGAT 600  
DB 541 CCGTCGCGCGCGCTTCTGATCCCACTGATGATGATGATGATGATGATGAT 600  
QY 601 CTTGCGCGCGGCGCTTCTGATGATGATGATGATGATGATGATGATGATG 660  
DB 601 CTTGCGCGCGGCGCTTCTGATGATGATGATGATGATGATGATGATGATG 660  
QY 661 TGCCTTCAACATGTCGATCATGATGATGATGATGATGATGATGATGATG 720  
DB 661 TGCCTTCAACATGTCGATCATGATGATGATGATGATGATGATGATGATG 720  
QY 721 ATACCGGCGCGGAGGCTGATGATGATGATGATGATGATGATGATGATG 780  
DB 721 ATACCGGCGCGGAGGCTGATGATGATGATGATGATGATGATGATGATG 780  
QY 781 GCTGCGCTTCTGTCGATGATGATGATGATGATGATGATGATGATGATG 840  
DB 781 GCTGCGCTTCTGTCGATGATGATGATGATGATGATGATGATGATGATG 840  
QY 841 CTTGATCCCGGAGGCGGAGGCTGATGATGATGATGATGATGATGATGATG 900  
DB 841 CTTGATCCCGGAGGCGGAGGCTGATGATGATGATGATGATGATGATGATG 900  
QY 901 GCGTTTCAACCTGAGATGATGATGATGATGATGATGATGATGATGATG 960  
DB 901 GCGTTTCAACCTGAGATGATGATGATGATGATGATGATGATGATGATG 960  
QY 961 CTAACCTGAACATGAGGCGGAGGCGGAGGCTGAGGCGGAGGCGGAGGCG 1020  
DB 961 CTAACCTGAACATGAGGCGGAGGCGGAGGCTGAGGCGGAGGCGGAGGCG 1020  
QY 1021 CCGCGAGCGCGCTCCGAGGCGGAGGCTGAGGCGGAGGCGGAGGCGGAGG 1080



```
Db 1021 CCCCCGACCCCTCCGAGGCCAGGCCCTACACCCCAACCCGCTGGCTGGGGCTG 1080
Qy 1081 CTGGCAGAAAGGGGCAAGGGAGGCCATGCCGCTGCAAGATATGGGTGGGTAGGGGCG 1140
Db 1081 CTGGCAGAAAGGGGCAAGGGAGGCCATGGCCGCTGCAAGATATGGGTGGGTAGGGGCG 1140
Qy 1141 CGTAGGCGCTGAGAGCGGGGGAGGGGAGCCCTCGGGGGGTGGGGGGGGGGCGGCTGG 1200
Db 1141 CGTAGGCGCTGAGAGCGGGGGAGGGGAGCCCTCGGGGGGTGGGGGGGGGGCGGCTGG 1200
Qy 1201 TTCACCACTCCAGCTCCGGGCAAGCTCTGAGAGGGGCACTGAGAGGCGCGCTCACTCA 1260
Db 1201 TTCACCACTCCAGCTCCGGGCAAGCTCTGAGAGGGGCACTGAGAGGCGCGCTCACTCA 1260
Qy 1261 GAGGGGCTCCAGAGCGGCTGGCGCTTCGGGCTTCGGTGGAGAGCGCATGAAATGGTGC 1320
Db 1261 GAGGGGCTCCAGAGCGGCTGGCGCTTCGGGCTTCGGTGGAGAGCGCATGAAATGGTGC 1320
Qy 1321 CCAGAGCTTCAACCAAGCGCTTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCT 1380
Db 1321 CCAGAGCTTCAACCAAGCGCTTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCT 1380
Qy 1381 CGTATCGTAGAGCATCTTGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCT 1440
Db 1381 CGTATCGTAGAGCATCTTGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCT 1440
Qy 1441 GGGCGGCTCGATGAGGCACTGCGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGG 1500
Db 1441 GGGCGGCTCGATGAGGCACTGCGCTTCGGGCTTCGGGCTTCGGGCTTCGGGCTTCGG 1500
Qy 1501 GTGGGCAACTCGGCTTCGCAACCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 1560
Db 1501 GTGGGCAACTCGGCTTCGCAACCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCT 1560
Qy 1561 GGGCTTCACCAAGAGCTCTGCGGCCCAAGAGAGCTCAAAATCAGAGCCCAAGCTCC 1620
Db 1561 GGGCTTCACCAAGAGCTCTGCGGCCCAAGAGAGCTCAAAATCAGAGCCCAAGCTCC 1620
Qy 1621 GCACTGCTGAGAGAGTGGGCGGCAAGAGAGCTCCCTCAGCGCAAGCGCTCTCAGCC 1680
Db 1621 GCACTGCTGAGAGAGTGGGCGGCAAGAGAGCTCCCTCAGCGCAAGCGCTCTCAGCC 1680
Qy 1681 GTCTCTGGGCACTGAGGCTTCGCTGCGGCCCTTACCGGCTGCTTCCCAAGGGTGA 1740
Db 1681 GTCTCTGGGCACTGAGGCTTCGCTGCGGCCCTTACCGGCTGCTTCCCAAGGGTGA 1740
Qy 1741 CGCGGCTGCTGAGGCTTCCTTAATGCAAGGAGAGCACTGCAATGAGAGGCGCTTC 1800
Db 1741 CGCGGCTGCTGAGGCTTCCTTAATGCAAGGAGAGCACTGCAATGAGAGGCGCTTC 1800
Qy 1801 CTGGGTTGGGCAAGAGGCGGCTTCAGTGGTGAAGTGGAGGCTGGGCGGCGCTTC 1860
Db 1801 CTGGGTTGGGCAAGAGGCGGCTTCAGTGGTGAAGTGGAGGCTGGGCGGCGCTTC 1860
Qy 1861 CCCACATTGCTGCTCAACCGGGAGAGGAGAGTGTGAGAGTCCAGATGCTGCCACCC 1920
Db 1861 CCCACATTGCTGCTCAACCGGGAGAGGAGAGTGTGAGAGTCCAGATGCTGCCACCC 1920
Qy 1921 CCGTGGTGGGCGCAACCTTCGAGTTAATGGTGGTGGTGGTGGTGGTGGTGGTGGT 1980
Db 1921 CCGTGGTGGGCGCAACCTTCGAGTTAATGGTGGTGGTGGTGGTGGTGGTGGTGGT 1980
Qy 1981 GTGTGCTCCAGGCTTCCTGCTAGAGAGTTGGCTTCGACAGTGGCAACAGCTGCACAC 2040
Db 1981 GTGTGCTCCAGGCTTCCTGCTAGAGAGTTGGCTTCGACAGTGGCAACAGCTGCACAC 2040
Qy 2041 CCGTGGCAACAGCTGCACAGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 2100
Db 2041 CCGTGGCAACAGCTGCACAGCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTCCTTC 2100
Qy 2101 CCTTGTGCTCTTGGCAATAGGCTCAGGCGTGGGCTTCGACCCCTTCGCAACACTCT 2160
Db 2101 CCTTGTGCTCTTGGCAATAGGCTCAGGCGTGGGCTTCGACCCCTTCGCAACACTCT 2160
```

```
Db 2101 CCTTGTGCTCTTGGCAATAGGCTCAGGCGTGGGCTTCGACCCCTTCGCAACACTCT 2160
Qy 2161 CTCTGCCCCCAAAAGTGTCAAGGGGCGCTTAAAGAACTCCAAAGTGTCTCTGCTTTCCA 2220
Db 2161 CTCTGCCCCCAAAAGTGTCAAGGGGCGCTTAAAGAACTCCAAAGTGTCTCTGCTTTCCA 2220
Qy 2221 TCTGGGTTGTTTCAAAAAGATGAAGAAACATGTCTGTGAATCTTGAATGTTGCGGG 2280
Db 2221 TCTGGGTTGTTTCAAAAAGATGAAGAAACATGTCTGTGAATCTTGAATGTTGCGGG 2280
Qy 2281 ATGTTAATCAAGAGAGCAAAATTCGTAGAGAGCTCAAGGCTGATATGGCAGGTGGG 2340
Db 2281 ATGTTAATCAAGAGAGCAAAATTCGTAGAGAGCTCAAGGCTGATATGGCAGGTGGG 2340
Qy 2341 CTCCCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
Db 2341 CTCCCAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400
Qy 2401 CACCCGCGCTGGGGCTCAACAGGCGCTGAGGCTCAAGGCTGAGTGGGCTGAGTGGT 2460
Db 2401 CACCCGCGCTGGGGCTCAACAGGCGCTGAGGCTCAAGGCTGAGTGGGCTGAGTGGT 2460
Qy 2461 GCTCAACCCAGAGACTCTGGGGGTTGTTGGAGAGAGGGGCGCCGCTGGGCGCAGGCT 2520
Db 2461 GCTCAACCCAGAGACTCTGGGGGTTGTTGGAGAGAGGGGCGCCGCTGGGCGCAGGCT 2520
Qy 2521 CAAGGCGTGCAGGGGCGGCTCAGAGAGAGTGGCCCGGCAAGGGCGCTTGGCAATGCT 2580
Db 2521 CAAGGCGTGCAGGGGCGGCTCAGAGAGAGTGGCCCGGCAAGGGCGCTTGGCAATGCT 2580
Qy 2581 GTGACACCGGCGGAGCGGCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Db 2581 GTGACACCGGCGGAGCGGCTGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2640
Qy 2641 AACCGTAGGTCACAAATTAAGTATTTTAAAAAATTTTAAAAAATTTTAAAAAATTT 2699
Db 2641 AACCGTAGGTCACAAATTAAGTATTTTAAAAAATTTTAAAAAATTTTAAAAAATTT 2699

RESULT 7
AD089179
ID AD089179 standard; cdna; 2699 BP.
XX
AC AD089179;
XX
XX 21-OCT-2004 (first entry)
XX
DE Human urological disorder related protein 8203 encoding cdna SEQ.131.
XX
KW urological disorder; uropathic; cytosstatic; urinary incontinence;
KW benign prostatic hyperplasia; human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 299..1636
FT /tag= a
FT /product= "urological disorder related protein 8203"
XX
PN MO2004065576-A2.
XX
PD 05-AUG-2004.
XX
PF 14-JAN-2004; 2004MO-US000750.
XX
PR 15-JAN-2003; 2003US-0440318P.
PR 04-FEB-2003; 2003US-0444783P.
PR 27-MAR-2003; 2003US-0457901P.
PR 08-MAY-2003; 2003US-0468775P.
PR 19-MAY-2003; 2003US-0471614P.
PR 16-JUN-2003; 2003US-0478742P.
PR 18-JUL-2003; 2003US-0488529P.
PR 30-JUL-2003; 2003US-0491156P.
```

PR 02-SEP-2003; 2003US-0499564P.  
PR 26-SEP-2003; 2003US-0506332P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Karicheci V, Silos-Santiago I, Eliasof SD.  
KA WPI: 2004-562167/54.  
DR P-PSDB; ADO89180.  
NR

PT Use of polypeptides related to urological disorders, e.g. 44390, 54181.  
PT 211 or for identifying a compound capable of treating a urological  
PT disorder or identifying and treating a subject having a urological  
PT disorder.

Claim 1; SEQ ID NO 131; 542pp; English.

The present invention describes the use of polypeptides related to urological disorders for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Also described: (1) a method for identifying a compound capable of treating a urological disorder; (2) a method for identifying a subject having a urological disorder; and (3) a method for treating a subject having a urological disorder. The compound has uropathic and cytosstatic activities. The polypeptides related to urological disorders are useful for identifying a compound capable of treating a urological disorder, identifying a subject having a urological disorder, or treating a subject having a urological disorder. Disorders include urinary incontinence and benign prostatic hyperplasia. The present sequence encodes a human urological disorder related protein, which is used in the exemplification of the present invention.

Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;

Query Match	100.0%	Score 2699	DB 13	Length 2699
Best Local Similarity	100.0%	Pred. NC. 0		
Matches 2699, Conservative	0	Mismatches	0	Indels 0; Gaps 0;

Qy	1	CCACGAGGTCGGCGCGCTGACAGGTGACACCGGACACGGGCTAGAGCTCCGCTCTCC	60
Db	1	CCACGAGGTCGGCGCGCTGACAGGTGACACCGGACACGGGCTAGAGCTCTCTCTCC	60
Qy	61	GCTGCAGACAGCGCGCTGCGCGGCCCCACTGAGGCTTGAGATCCGAGCCCGGCCCCCTCGGCA	120
Db	61	GCTGCAGACAGCGCGCTGCGCGGCCCCACTGAGGCTTGAGATCCGAGCCCGGCCCCCTCGGCA	120
Qy	121	CGGCTGCTTGAGCCCGCGGCCCCCGGCGCGGACGATGCGCTGAGCGCGCCCCAGGGAA	180
Db	121	CGGCTGCTTGAGCCCGCGGCCCCCGGCGCGGACGATGCGCTGAGCGCGCCCCAGGGAA	180
Qy	181	ACCCGACCCGGGCCAAGAGGGCCGGCAAAAGACGAGGCTCCGGGCGGGGCGCTCTCCGGCGG	240
Db	181	ACCCGACCCGGGCCAAGAGGGCCGGCAAAAGACGAGGCTCCGGGCGGGGCGCTCTCCGGCGG	240
Qy	241	CCGAGCTCTCGGCGCGCGCTTGCGCCCGGCGTCCGGACCCGCGTAGCGCTGCGGGGCGCAT	300
Db	241	CCGAGCTCTCGGCGCGCGCTTGCGCCCGGCGTCCGGACCCGCGTAGCGCTGCGGGGCGCAT	300
Qy	301	GGAGCGCGCGCGCGCCGACGAGCGGCGCGCTTTCGGGGGCGCTGCGCGGCGATGCGGC	360
Db	301	GGAGCGCGCGCGCGCCGACGAGCGGCGCGCTTTCGGGGGCGCTGCGCGGCGATGCGGC	360
Qy	361	GGGGGGGGGCGGGGGCGGGGGCTTTCGCGGACGCTGACCGCGGTCGTGGCGGCTCAT	420
Db	361	GGGGGGGGGCGGGGGCGGGGGCTTTCGCGGACGCTGACCGCGGTCGTGGCGGCTCAT	420
Qy	421	GGCGCTCATCGTGGGCCACGGTCTGGGCAACGCGCTGCTCATGCTCGCTTCGTGGC	480
Db	421	GGCGCTCATCGTGGGCCACGGTCTGGGCAACGCGCTGCTCATGCTCGCTTCGTGGC	480
Qy	481	CGAGTCGAGCTTCGCAACCCAGAACACTTCTCTGCTCAACTCGGCATCTTCGACTT	540



181 ACCGACCCGGCCAAAGGGCCCGCAAAAGAGGCTCCGGGCGGGGCCCTCCGGCCG 240  
181 ACCCGACCCGGCCAAAGGGCCCGCAAAAGAGGCTCCGGGCGGGGCCCTCCGGCCG 240  
241 CCCAGCTCTGCGCGGGGCCCTGCCCCGGCTCCGGAGCCCGGTGAGCTCGGGGCCAT 300  
241 CCCAGCTCTGCGCGGGGCCCTGCCCCGGCTCCGGAGCCCGGTGAGCTCGGGGCCAT 300  
301 GGAGCGCGCGCGCCCGAGCGGGCGGTGAAACGCTTGCGGGGGCGCTGCGGGCGAGTGGAG 360  
301 GGAGCGCGCGCGCCCGAGCGGGCGGTGAAACGCTTGCGGGGGCGCTGCGGGCGAGTGGAG 360  
361 GCGCGCGCGCGGGCGCGGGCTTCTGCGAGCGCTTGAGACCGCGGTGCTGAGCGCGCTCAT 420  
361 GCGCGCGCGCGGGCGCGGGCTTCTGCGAGCGCTTGAGACCGCGGTGCTGAGCGCGCTCAT 420  
421 GCGCGCTGCTATCTGTGGCCACCGGTGCTGGGCAACGCGGTGCTATCTGCGCTTCTGTGGC 480  
421 GCGCGCTGCTATCTGTGGCCACCGGTGCTGGGCAACGCGGTGCTATCTGCGCTTCTGTGGC 480  
481 CGAGCTGAGCTCTCGGACCCAGAACAACTTCTTCTGCTCAACCTGCGCATCTCGGACTT 540  
481 CGAGCTGAGCTCTCGGACCCAGAACAACTTCTTCTGCTCAACCTGCGCATCTCGGACTT 540  
541 CCTGCTCGCGCGCTTCTGCACTCCACTGATGTAACCTTACGTGCTGACAGAGCGCGTGGAC 600  
541 CCTGCTCGCGCGCTTCTGCACTCCACTGATGTAACCTTACGTGCTGACAGAGCGCGTGGAC 600  
601 CTTGCGCGCGGGCTCTGCAAGCTGTGGCTGTGATGTAACCTGCTGTGACACTCTCTC 660  
601 CTTGCGCGCGGGCTCTGCAAGCTGTGGCTGTGATGTAACCTGCTGTGACACTCTCTC 660  
661 TGCTTCAACATGTGCTGATCAGCTACGACGCTTCTGCTGCTGATACCGGAGCGGCTCTC 720  
661 TGCTTCAACATGTGCTGATCAGCTACGACGCTTCTGCTGCTGATACCGGAGCGGCTCTC 720  
721 ATACCGGGCCCAAGAGGTGACACGCGCGGGCGAGTGGCGGAAGATCTGCTGTGGGT 780  
721 ATACCGGGCCCAAGAGGTGACACGCGCGGGCGAGTGGCGGAAGATCTGCTGTGGGT 780  
781 GCTGCGCTTCTGCTGTGATGAGACCAAGCATCTGAGCTGGAGATCTCTGCGGGGCCAG 840  
781 GCTGCGCTTCTGCTGTGATGAGACCAAGCATCTGAGCTGGAGATCTCTGCGGGGCCAG 840  
841 CTCGATCCCCGAGGGCCACGTGATGCGAGTCTTCTCAACTGTGATCTCTCATAC 900  
841 CTCGATCCCCGAGGGCCACGTGATGCGAGTCTTCTCAACTGTGATCTCTCATAC 900  
901 GCGCTTCAACCTGAGATTCTTTACGCGCTTCTCAGCGTACACTTCTTTAACTCAGCAT 960  
901 GCGCTTCAACCTGAGATTCTTTACGCGCTTCTCAGCGTACACTTCTTTAACTCAGCAT 960  
961 CTAAGCTGAACATCAAGAGGCGCACCGCGCTCCGGCTGAGTGGGGCTCGAAGAGCACCCG 1020  
961 CTAAGCTGAACATCAAGAGGCGCACCGCGCTCCGGCTGAGTGGGGCTCGAAGAGCACCCG 1020  
1021 CCGCGAGCGCGCTCCCGAGGGCCAGGCTCAACCGCCCAACCGCGCTGCGTGGGGCTG 1080  
1021 CCGCGAGCGCGCTCCCGAGGGCCAGGCTCAACCGCCCAACCGCGCTGCGTGGGGCTG 1080  
1081 CTGGCGAAGGGGCAACGGGAGGCGCATGCGCTGCAAGGTATGGGGTGGGTGAGCGCGC 1140  
1081 CTGGCGAAGGGGCAACGGGAGGCGCATGCGCTGCAAGGTATGGGGTGGGTGAGCGCGC 1140  
1141 CGTAGCGCTGAGGCGCGGAGGCGACCTCTCGGGGCTGGCGGGCGGCTCGGTGAC 1200  
1141 CGTAGCGCTGAGGCGCGGAGGCGACCTCTCGGGGCTGGCGGGCGGCTCGGTGAC 1200  
1201 TTCAACCACTTCAGAGTCCGGGAGCTCTCGAGGGGCACTGAGAGGCGCGGCTCACTCAA 1260  
1201 TTCAACCACTTCAGAGTCCGGGAGCTCTCGAGGGGCACTGAGAGGCGCGGCTCACTCAA 1260

1261 GAGGGCTTCAAGCCGTGCGCTCTCGGCTCTGCTGAGAAAGCGCATGAGATGCTGTC 1320  
1261 GAGGGCTTCAAGCCGTGCGCTCTCGGCTCTGCTGAGAAAGCGCATGAGATGCTGTC 1320  
1321 CCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTGGGACAGGAAAGTGGCCAACTCGCTGC 1380  
1321 CCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTGGGACAGGAAAGTGGCCAACTCGCTGC 1380  
1381 CGTCAATGAGACATCTTTGAGGCTCTGCTGGGCCCCA7CAGCGCTGATGATCATCCG 1440  
1381 CGTCAATGAGACATCTTTGAGGCTCTGCTGGGCCCCA7CAGCGCTGATGATCATCCG 1440  
1441 GCGCGCTTCCATGCGCACTGCGCTCTGATCTGATCTGATGTAACAACTCTTCTGCTCT 1500  
1441 GCGCGCTTCCATGCGCACTGCGCTCTGATCTGATCTGATGTAACAACTCTTCTGCTCT 1500  
1501 GCGCGCTTCCATGCGCACTGCGCTCTGATCTGATCTGATGTAACAACTCTTCTGCTCT 1560  
1501 GCGCGCTTCCATGCGCACTGCGCTCTGATCTGATCTGATGTAACAACTCTTCTGCTCT 1560  
1561 GCGCTTCAACCAAGCTTCTGCGCCCAAGAGCTCAAAATCCAGCCCAAGCTCCCTGGA 1620  
1561 GCGCTTCAACCAAGCTTCTGCGCCCAAGAGCTCAAAATCCAGCCCAAGCTCCCTGGA 1620  
1621 GCACTGTGGAAGTGAAGTGGCCACACAGAGCTCCCTCAGCCAGCGCTCTCTCAAGCCAG 1680  
1621 GCACTGTGGAAGTGAAGTGGCCACACAGAGCTCCCTCAGCCAGCGCTCTCTCAAGCCAG 1680  
1681 GTCTCTGGGCAATCTGAGCTGCTGCTCCCTTACCCGGCTCTGTTCCCGGGGTGAGCC 1740  
1681 GTCTCTGGGCAATCTGAGCTGCTGCTCCCTTACCCGGCTCTGTTCCCGGGGTGAGCC 1740  
1741 GCGCGCTTCTGAGCGCTCTCTTTAAATGCAAGGAGCCACCTGCGCATGAGAGCGCTTC 1800  
1741 GCGCGCTTCTGAGCGCTCTCTTTAAATGCAAGGAGCCACCTGCGCATGAGAGCGCTTC 1800  
1801 CTGGGTTGGCCAGAGGGCCCTTCACTGCTGGAATGGAAGTGGGTGGCGGCGCTTCCC 1860  
1801 CTGGGTTGGCCAGAGGGCCCTTCACTGCTGGAATGGAAGTGGGTGGCGGCGCTTCCC 1860  
1861 CCGCAATTTGGCTCCACCGGGGAGGACAGTCTGAGGTCCCAACATGCTGCCACCC 1920  
1861 CCGCAATTTGGCTCCACCGGGGAGGACAGTCTGAGGTCCCAACATGCTGCCACCC 1920  
1921 CCGCTGAGGCGCCACCTTCCAGATTACTGTTGATGTTCTTCCAAAGCAAGCACTGG 1980  
1921 CCGCTGAGGCGCCACCTTCCAGATTACTGTTGATGTTCTTCCAAAGCAAGCACTGG 1980  
1981 GTGTGCTCCAGGCTTCTGCTGCTAGACGTTTGGCTCTGTGACAGTGCACACCTGCACAC 2040  
1981 GTGTGCTCCAGGCTTCTGCTGCTAGACGTTTGGCTCTGTGACAGTGCACACCTGCACAC 2040  
2041 CCGTGCACACCTGACACACCGTCCCTTCCCGGACCAAGCCCAAGACATGTGCTTGGCTG 2100  
2041 CCGTGCACACCTGACACACCGTCCCTTCCCGGACCAAGCCCAAGACATGTGCTTGGCTG 2100  
2101 CCGTGTGCTCTTGTGACATGAGCTCAGAGCTGAGCTTCAACCCCTTCCCAACACTCT 2160  
2101 CCGTGTGCTCTTGTGACATGAGCTCAGAGCTGAGCTTCAACCCCTTCCCAACACTCT 2160  
2161 CTCTGCCCCCAAAAGTGTCAAGGGGCGCTTGAAGAACTGGAACCTGTCTCTCTTTTCA 2220  
2161 CTCTGCCCCCAAAAGTGTCAAGGGGCGCTTGAAGAACTGGAACCTGTCTCTCTTTTCA 2220  
2221 TTCTGGGTCTTTTCAAGAAAGATGAAGAAACATGTCTGGAATCTGATGTGTGGG 2280  
2221 TTCTGGGTCTTTTCAAGAAAGATGAAGAAACATGTCTGGAATCTGATGTGTGGG 2280  
2281 ATGTTTAATCAAGAGAGCAAAATTTCTGAGAGGCTCAGGGCTGAGTTGGCAGGTGGG 2340  
2281 ATGTTTAATCAAGAGAGCAAAATTTCTGAGAGGCTCAGGGCTGAGTTGGCAGGTGGG 2340  
2341 CTCACAGCGCTCTCTCCCTCCGCTTAAGGCTTCCGCTGAGTGTGCAGCTGCTTCTGCGC 2400

|||||  
DB 2341 CTCGCAAGCCCTCTCCCTCCGTAAGGCTTCGGGCTGAGCTGTGCGAGCTGCTTCC 2400  
QY 2401 CACCCCGCTCTGGGCTCACACAGCCCTGTGTGGCCAAAGCTTCCCGGCACTGTGTTT 2460  
DB 2401 CACCCCGCTCTGGGCTCACACAGCCCTGTGTGGCCAAAGCTTCCCGGCACTGTGTTT 2460  
QY 2461 GCTCACCGAGGACTCTGGGGGTTGTTGGAGAGAGGGGGCCCGCTGGGCGCAGGGTTC 2520  
DB 2461 GCTCACCGAGGACTCTGGGGGTTGTTGGAGAGAGGGGGCCCGCTGGGCGCAGGGTTC 2520  
QY 2521 CAAGGCTGACAGGGGGGCTTCAGAGAGAGTCCCGGCGCAGGGGCGCTTGGCATGTGCT 2580  
DB 2521 CAAGGCTGACAGGGGGGCTTCAGAGAGAGTCCCGGCGCAGGGGCGCTTGGCATGTGCT 2580  
QY 2581 GTGACACCCGTGACAGCGGCTGTGATGCTCTCTGCTGTGCTGCTGCGCTGCTGCA 2640  
DB 2581 GTGACACCCGTGACAGCGGCTGTGATGCTCTCTGCTGTGCTGCTGCGCTGCTGCA 2640  
QY 2641 AACCGAGGTCACATTAAGTATTTTAAAAA 2699  
DB 2641 AACCGAGGTCACATTAAGTATTTTAAAAA 2699  
RESULT 9  
AAK02885  
ID AAK02885 standard; cDNA; 2689 BP.  
XX  
AC AAK02885;  
XX  
DT 17-MAY-1999 (first entry)  
XX  
DE Human mAChR-6 cDNA.  
XX  
KM mAChR-6; muscarinic acetylcholine receptor 6; disorder; secretion;  
KM acetylcholine responsive cell; phosphatidylinositol turn-over;  
KM smooth muscle cell contraction; nervous system disorder; glandular;  
KM schizo-affective disorder; affective disorder; sleep disorder;  
KM movement disorder; eating disorder; drinking disorder; human; 89.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 291..1628  
FT /\*tag= a  
FT /product= "mAChR-6"  
XX  
PN US5882893-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 04-DEC-1997; 97US-00985090.  
XX  
PR 04-DEC-1997; 97US-00985090.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Goodearl AD;  
XX  
PI WPI; 1999-214063/18.  
XX  
DR P-PSDB; AAW92975.  
XX  
PT Nucleic acids encoding muscarinic acetylcholine receptor 6 - useful for  
PT modulating the effects of acetylcholine on acetylcholine responsive  
PT cells.  
XX  
PS Claim 23; Fig 1A-D; 59pp; English.  
XX  
CC This invention describes the isolation of a novel human muscarinic  
CC acetylcholine receptor 6 (mAChR-6), capable of modulating the effects of  
CC acetylcholine on acetylcholine responsive cells. mAChR-6 cDNAs and  
CC polypeptides may be used to detect naturally occurring mutations of the  
CC mAChR-6 gene and determine if a subject with the mutated gene is at risk

CC of (or is predisposed to have) a mAChR-6 related disorder, modulate cell  
CC activity mediated by mAChR-6 (e.g. biological processes mediated by  
CC phosphatidylinositol turn-over and signalling), secretion of a molecule  
CC (e.g. a neurotransmitter or a glandular enzyme), or contraction of a  
CC smooth muscle cell, treat disorders mediated by abnormal mAChR-6 activity  
CC e.g. nervous system disorders (e.g. amnesia, apraxia, agnosia, amnesic  
CC dysnomia), amnesic spatial disorientation, Kluver-Bucy syndrome,  
CC Alzheimer's related memory loss and learning disability, visual  
CC hallucinations, perceptual disturbances, and Lewy body dementia  
CC associated delirium), schizo-affective disorders (e.g. schizophrenia with  
CC mood swings, and depressive illness), affective disorders, sleep  
CC disorders (e.g. REM sleep abnormalities, paradoxical sleep abnormalities,  
CC sleep-wakefulness, and body temperature or respiratory depression  
CC abnormalities during sleep), pain generating mechanism disorders (e.g.  
CC related to irritable bowel syndrome (IBS), or chest pain), movement  
CC disorders (e.g. related to Parkinson's disease), eating disorders (e.g.  
CC insulin hypersecretion related obesity), drinking disorders (e.g.  
CC diabetic polydipsia), smooth muscle related disorders (e.g. IBS,  
CC diverticular disease, urinary incontinence, oesophageal achalasia, and  
CC chronic obstructive airways disease), cardiac disorders (e.g. pathologic  
CC bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and  
CC glandular disorders (e.g. xerostomia and diabetes mellitus)  
XX  
SQ Sequence 2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;

Query Match 97.6%; Score 2635.2; DB 2; Length 2689;

Best Local Similarity 99.8%; Pred. No. 0; Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 25 CGCAGCCGACAGCGGCTCAGGCTCCGCTCTCTCCGCTGACAGACCGGCTGCGGGCC 84  
DB 18 CGCAGCCGACAGCGGCTCAGGCTCCGCTCTCTCCGCTGACAGACCGGCTGCGGGCC 77  
QY 85 CCACTGAGCTCGGATCCGGCCCCCGCTCGGACCGCTGCTGTGCTCCCGGCCG 144  
DB 78 CCACTGAGCTCGGATCCGGCCCCCGCTCGGACCGCTGCTGTGCTCCCGGCCG 137  
QY 145 GCGCCCGGACCAATGCGGTGCGGGGCGCCCGACGGGGAACCGACCGGCGCAAGGGCCGCA 204  
DB 138 GCGCCCGGACCAATGCGGTGCGGGGCGCCCGACGGGGAACCGACCGGCGCAAGGGCCGCA 196  
QY 205 AAGACGAGGCTCCGAGGCGGGGCGCCCTCCGCGCGCCGACGCTCTGCGCGGCGCTGCG 264  
DB 197 AAGACGAGGCTCCGAGGCGGGGCGCCCTCCGCGCGCCGACGCTCTGCGCGGCGCTGCG 256  
QY 265 CCGCGCTCCGAGCGCGCTGAGCTTCCGAGGCGCATGAGAGCGCGCGCCGCAAGGGCC 324  
DB 257 CCGCGCTCCGAGCGCGCTGAGCTTCCGAGGCGCATGAGAGCGCGCGCCGCAAGGGCC 316  
QY 325 GCTGAACGCTTCGGGGGCGCTGCGCGGCGCATGCGGCGCGCGGGCGGGCGGCGCTT 384  
DB 317 GCTGAACGCTTCGGGGGCGCTGCGCGGCGCATGCGGCGCGGGCGGGCGGGCGGCGCTT 376  
QY 385 CTCGAGAGCTTGAGACCGGCTGCGCGGCGCTCATGAGCGCTCTCATGCTGAGCGCAAGT 444  
DB 377 CTCGAGAGCTTGAGACCGGCTGCGCGGCGCTCATGAGCGCTCTCATGCTGAGCGCAAGT 436  
QY 445 GCTGGGCAACGCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 504  
DB 437 GCTGGGCAACGCGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 496  
QY 505 CAACCTTCTTCGCTCAACCTGCGCATTCGCGCTTCGCTGCGGGCGCTTTCGCAATCC 564  
DB 497 CAACCTTCTTCGCTCAACCTGCGCATTCGCGCTTCGCTGCGGGCGCTTTCGCAATCC 556  
QY 565 ACTGATGTAACCTTACGCTGCTGACAGGCGCTGACGCTTTCGCGGGCGCTTTCGCAAGCT 624  
DB 557 ACTGATGTAACCTTACGCTGCTGACAGGCGCTGACGCTTTCGCGGGCGCTTTCGCAAGCT 616  
QY 625 GTGGCTGTGATGAGACTACCTGCTGTGACACTTCTCTGCTTCAACATGCTGTCAATGAG 664  
DB 617 GTGGCTGTGATGAGACTACCTGCTGTGACACTTCTCTGCTTCAACATGCTGTCAATGAG 676

OY	685	TTACGACCGCGTTCCTGTCGAGTACCCGAGCGGTCTCATACCGGGCCAGCAGGGGTAC	744
Db	677	CTACGACCGGCTTCCTGTCGTCACCCGAGCGGTCTCATACCGGGCCAGCAGGGGTAC	736
OY	745	GCGGCGGGCAGTCGCGAAGATGCTGCTGATGAGGTGTGGCTCTTCCGTGTACGAGC	804
Db	737	GCGGCGGGCAGTCGCGAAGATGCTGCTGATGAGGTGTGGCTCTTCCGTGTACGAGC	796
OY	805	AGCCATCTGAGCTGGAGTACTGTCCGGGGCAGCTTCATTCCCGAGGGCCACTGCTA	864
Db	797	AGCCATCTGAGCTGGAGTACTGTCCGGGGCAGCTTCATTCCCGAGGGCCACTGCTA	856
OY	865	TGCCGAGTTCTTTCACATGTAATCTTCTCATCAACGGCTTCCACCCGTGAGTCTTTAC	924
Db	857	TGCCGAGTTCTTTCACATGTAATCTTCTCATCAACGGCTTCCACCCGTGAGTCTTTAC	916
OY	925	GCCCTCTCTCAGCGTCACCTTCTTTCACCTGAGCATCTACCTGAAATCCAGAGCGCAC	984
Db	917	GCCCTCTCTCAGCGTCACCTTCTTTCACCTGAGCATCTACCTGAAATCCAGAGCGCAC	976
OY	985	CCGCTCTCGGCTGGATGGGGCTCGAGAGGCAGCCGGCCCCGAGGCCCTCCGAGGCCA	1044
Db	977	CCGCTCTCGGCTGGATGGGGCTCGAGAGGCAGCCGGCCCCGAGGCCCTCCGAGGCCA	1036
OY	1045	GCCCTCACACCCCCACCGCCTGCTGGGGGCTGTGGGAGAAAGGGGCAACGGGGAGGC	1104
Db	1037	GCCCTCACACCCCCACCGCCTGCTGGGGGCTGTGGGAGAAAGGGGCAACGGGGAGGC	1096
OY	1105	CATGCGCGTGCACAGGTATGGGGGTGGGTGAGAGCGGCGTAGGCGCTGAGGCGGGAGGC	1164
Db	1097	CATGCGCGTGCACAGGTATGGGGGTGGGTGAGAGCGGCGTAGGCGCTGAGGCGGGAGGC	1156
OY	1165	GACCTCGGGGGGTGGCGGTTGGGGGCGGCTCCGTGGCTTACCCACCTTCAGCTCCGAG	1224
Db	1157	GACCTCGGGGGGTGGCGGTTGGGGGCGGCTCCGTGGCTTACCCACCTTCAGCTCCGAG	1216
OY	1225	CTCTCTGAGGGGCACTGAGAGGCGCGCTCACTCAAGGGGCTTCAAGCCGTGGGCTC	1284
Db	1217	CTCTCTGAGGGGCACTGAGAGGCGCGCTCACTCAAGGGGCTTCAAGCCGTGGGCTC	1276
OY	1285	CTGGGCTCGCTGGAGAGCGCATTAATGATGTCACGAGGCTTCAACCAGCGTTTCG	1344
Db	1277	CTGGGCTCGCTGGAGAGCGCATTAATGATGTCACGAGGCTTCAACCAGCGTTTCG	1336
OY	1345	GCTGCTTCGGGACAGAGAAATGGCCAAATCGCTGGCCGTGCATCTGTAGCATTTTGGGCT	1404
Db	1337	GCTGCTTCGGGACAGAGAAATGGCCAAATCGCTGGCCGTGCATCTGTAGCATTTTGGGCT	1396
OY	1405	CTGCTGGGCCCCCATATCAGCTGTGTATATCATTCGGGCGCTGSCCATGSCCATCTGCT	1464
Db	1397	CTGCTGGGCCCCCATATCAGCTGTGTATATCATTCGGGCGCGCTGSCCATATGSCCATCTGCT	1456
OY	1465	CCCTGACTACTGATGTCGAAACCTCTCTTGGGCTCTGTGGGCAACTGGGCGTCAACC	1524
Db	1457	CCCTGACTACTGATGTCGAAACCTCTCTTGGGCTCTGTGGGCAACTGGGCGTCAACC	1516
OY	1525	TGTCCTTACCTCTGTGSCACACACAGCTTCGCGGGGCTTTCACCAAGCTGCTTGCC	1584
Db	1517	TGTCCTTACCTCTGTGSCACACACAGCTTCGCGGGGCTTTCACCAAGCTGCTTGCC	1576
OY	1585	CCAGAGGCTCAAAATTCAGGCCACACAGCTCCTTGAGACATGTCTGGAAGTGAATGGCCCA	1644
Db	1577	CCAGAGGCTCAAAATTCAGGCCACACAGCTCCTTGAGACATGTCTGGAAGTGAATGGCCCA	1636
OY	1645	CCAGAGGCTCCTCAGCAGCGCTCTCAGCCAGGCTCTCTGGGCACTTGGGCGCTGSC	1704
Db	1637	CCAGAGGCTCCTCAGCAGCGCTCTCAGCCAGGCTCTCTGGGCACTTGGGCGCTGSC	1696
OY	1705	GCCCCCTACCGGCTGTTCCCCAGGGGTGAGCCCGCCGATGTGTGGCCCTTCTTTA	1764
Db	1697	GCCCCCTACCGGCTGTTCCCCAGGGGTGAGCCCGCCGATGTGTGGCCCTTCTTTA	1756
OY	1765	ATGCCACGGACGACCCCTGCAATGAGGCGCTTCTGTGGTTGGCAGAGGGCCCTTCA	1824

Db	1757	ATGTCACAGGCAACCCCTTGCTGCATGAGAGCGCCCTTCTCTGGGTGGCCAGAGGGCCCTCTCA	1816
Oy	1825	CTGGCTGACCTGAGAGGCTGGGTGGCCGGCCCTCTGCCCCCAATCTTG3CTTCAACCG3GGA	1884
Db	1817	CTGGCTGGAAGTGAGGCTGGGGTGGCCGGCCCTGCGCCCCACACTTG6GCTCACCC -GGGA	1875
Oy	1885	GGGACAGCTGTGAGAGGTCCCAAGACATGCTGCCCAACCCCTCTGTGGTGGCCACCTTCCGAG	1944
Db	1876	GGGACAGCTGTGAGAGGTCCCAAGACATGCTGCCCAACCCCTCTGTGGTGGCCACCTTCCGAG	1935
Oy	1945	TTACTGTGGTGGTGTCTTCTCCAAAGACAAGCACTGGGGTGTGCTCAAG3CTTCTGCCCCCTA	2004
Db	1936	TTACTGTGGTGGTGTCTTCTCCAAAGACAAGCACTGGGGTGTGCTCAAG3CTTCTGCCCCCTA	1995
Oy	2005	GCAAGTTTGCCCTCTGACAGTGCACACACTGACACCCCTGACACACCTGACACACCTGC	2064
Db	1996	GCAAGTTTGCCCTCTGACAGTGCACACACTGACACCCCTGACACACCTGACACACCTGC	2055
Oy	2065	CTCTCCCCCGACAAAGCCCAAGACATGCTCTTGTGTGCTTCTGTCTCTTGATTAAGCTC	2124
Db	2056	CTCTCCCCCGACAAAGCCCAAGACATGCTCTTGTGTGCTTCTGTCTCTTGATTAAGCTC	2115
Oy	2125	AGGCTGTGACCCCTTTCACCCCTCTTCCCAACCACTCTCTGACCCCAAAAGTGCAGAGG	2184
Db	2116	AGGCTGTGACCCCTTTCACCCCTCTTCCCAACCACTCTCTGACCCCAAAAGTGCAGAGG	2175
Oy	2185	GCCCTAGGAACCTTGAAGCTGTGCTCTGCTTTTCATCTTGAGGTGTTTCAGAAAGTGA	2244
Db	2176	GCCCTAGGAACCTTGAAGCTGTGCTCTGCTTTTCATCTTGAGGTGTTTCAGAAAGTGA	2235
Oy	2245	AGAGAAAACATGCTCTGAACTTGATGTTCTGTGGATGTTTAAATCAAGAGACAAAT	2304
Db	2236	AGAGAAAACATGCTCTGAACTTGATGTTCTGTGGATGTTTAAATCAAGAGACAAAT	2295
Oy	2305	TGCTGAGGAGCTCAGGGCTGGATTGGAGAGGTGGAGCTCCAGAGCCCTCTCCCTCGGCT	2364
Db	2296	TGCTGAGGAGCTCAGGGCTGGATTGGAGAGGTGGAGCTCCAGAGCCCTCTCCCTCGGCT	2355
Oy	2365	AAGGCTTCCGCTGAGCTGTGTCAGACTCTTCTGACCAACCCCGCTCTGGGCTCACACA	2424
Db	2356	AAGGCTTCCGCTGAGCTGTGTCAGACTCTTCTGACCAACCCCGCTCTGGGCTCACACA	2415
Oy	2425	GCCCTGTGTCAGAACCTGCTGCCCGGCACTCTGTTTGTCTACCAAGACCTCTGGGGGT	2484
Db	2416	GCCCTGTGTCAGAACCTGCTGCCCGGCACTCTGTTTGTCTACCAAGACCTCTGGGGGT	2475
Oy	2485	GTTGGGAGAGAGGGGGCCGCGCTGGGGCCGAGGGGTCCAAAGGCTGCAAGGGGGGTCCAGA	2544
Db	2476	GTTGGGAGAGAGGGGGCCGCGCTGGGGCCGAGGGGTCCAAAGGCTGCAAGGGGGGTCCAGA	2535
Oy	2545	GGAAGTCCCGGAGGAGGGCCGCTTTCGCAATGTGCTGTGCAACCGTGCACGCGCTCTGC	2604
Db	2536	GGAAGTCCCGGAGGAGGGCCGCTTTCGCAATGTGCTGTGCAACCGTGCACGCGCTCTGC	2595
Oy	2605	ATGCTCTCTGCTGTGCTGCGCGCTGCGCTGCGCTGCGCAAAACGCTGAGGTCAATTAAGTGT	2664
Db	2596	ATGCTCTCTGCTGTGCTGCGCGCTGCGCTGCGCTGCGCAAAACGCTGAGGTCAATTAAGTGT	2655
Oy	2665	ATTTTTTTTAAAAAATTTTTTTTTT 2688	
Db	2656	ATTTTTTTTAAAAAATTTTTTTTTT 2679	
RESULT 10			
AAK59167			
ID	AAK59167 standard; cDNA; 2689 BP.		
XX	AAK59167;		
AC			
XX			
DT	06-SEP-1999 (first entry)		
DE	Human G protein coupled receptor flh8495 cDNA.		

XX G protein coupled receptor; flh8495; human; diagnosis; screening;  
KW therapy; antiparkinsonian; nootropic; neuroprotective; neuroplastic;  
KW antidepressant; antiarrhythmic; antidiabetic; antiinflammatory;  
KW phosphatidylinositol; ss.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX CDS 291..1628  
XX /tag= a  
XX /note= "this region is specifically claimed in claim 7a"  
XX  
XX MO928470-A1.  
XX  
XX 10-JUN-1999.  
XX  
XX 04-DEC-1998; 98WO-US025832.  
XX  
XX 04-DEC-1997; 97US-00985090.  
XX 17-MAR-1998; 98US-00042780.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Goodearl ADJ, Gluckmann MA, Xie M, Dietefano P;  
XX WPI, 1999-394858/33.  
XX P-SDB; AA106322.  
XX  
XX New nucleic acid encoding an isolated G-protein coupled receptor useful  
XX for treating nervous system related disorders.  
XX  
XX Claim 7a; Fig 1; 140pp; English.  
XX  
XX This nucleotide sequence, the coding region of which is claimed, codes  
XX for a novel human G protein coupled receptor, termed flh8495 (see  
XX AA106322). The flh8495 cDNA was identified in a human cerebellum cDNA  
XX library using a rat flh8495 fragment (see also AAX59168) as probe. The  
XX invention provides human, rat and mouse flh8495 polynucleotides  
XX (including polynucleotides encoding the transmembrane regions of flh8495  
XX and antisense nucleic acid molecules), expression vectors, host cells,  
XX transgenic animals, flh8495 polypeptides and antibodies, and a method of  
XX modulating phosphatidylinositol metabolism. The flh8495 polypeptides can  
XX (i) interact with a flh8495 ligand, such as acetylcholine or carntine,  
XX (ii) interact with a G protein or another protein which naturally binds  
XX to flh8495, (iii) modulate the activity of an ion channel (e.g. a calcium  
XX activated chloride channel or a potassium or calcium channel), (iv)  
XX modulate cytosolic ion, e.g. calcium concentration, (v) modulate the  
XX release of a neurotransmitter, e.g. acetylcholine or carnitine from a  
XX neuron, (vi) modulate a flh8495 ligand response in a responsive cell,  
XX (vii) signal ligand binding via phosphatidylinositol turnover, and (viii)  
XX modulate phospholipase C activity. The products can be used to treat:  
XX disorders mediated by abnormal flh8495 polypeptide activity such as  
XX nervous system related disorders e.g. amnesia, apraxia, agnosia,  
XX Alzheimer's related memory loss and learning disability; disorders  
XX affecting consciousness such as visual hallucinations, peteputal  
XX disturbances or delirium associated with Lewy body dementia, schitzo-  
XX effective disorders, schizophrenia with mood swings, depressive illness  
XX (primary and secondary); affective disorders such as REM sleep  
XX abnormalities in patients suffering from e.g. depression, parodoxical  
XX sleep abnormalities, sleep-wakefulness, and body temperature or  
XX respiratory depression abnormalities during sleep; disorders affecting  
XX pain generation mechanisms e.g. pain related to irritable bowel syndrome  
XX or chest pain; movement disorders e.g. Parkinson's disease related  
XX movement disorders; eating disorders e.g. insulin hypersecretion related  
XX obesity or drinking disorders, e.g. diabetic polydipsia; smooth muscle  
XX related disorders, e.g. irritable bowel syndrome, diverticular disease,  
XX urinary incontinence, oesophageal achalasia or chronic obstructive  
XX airways disease; cardiac muscle disorders, e.g. pathological bradycardia or  
XX tachycardia, arrhythmia, flutter or fibrillation; and gland related  
XX disorder such as xerostomia or diabetes mellitus. The products can also  
XX be used for detection, diagnosis and drug screening

XX  
SQ Sequence 2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;  
Query Match 97.6%; Score 2635.2; DB 2; Length 2689;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
QY  
25 CGCACCAGGAGCGGCTCAGAGCTCCGCTCTCTCCGCTGACAGCAGCGGCTGCGGCGC 84  
DB CGCACCAGGAGCGGCTCAGAGCTCCGCTCTCTCTCCGCTGACAGCAGCGGCTGCGGCGC 77  
QY CCACTGAGGCTCGAGTCCGAGCCCGGCGCCCTCGCGACCGCTGCTGCGCCCGGCGCG 144  
DB CCACTGAGGCTCGAGTCCGAGCCCGGCGCCCTCGCGACCGCTGCTGCGCCCGGCGCG 137  
QY 145 GCCCGCGGACCATGCGCTGAGGCGCCCGGAGGAGAAACCGACCCGAGCGGCGCGCA 204  
DB GCCCGCGGACCATGCGCTGAGGCGCCCGGAGGAGG -AACCGACCCGAGCGGCGCGCA 196  
QY 205 AAGACGAGGCTCCCGGCGCGGCGCCCTCGCGCGCGCCAGCTTGAGGCGGCGCGCTGC 264  
DB AAGACGAGGCTCCCGGCGCGGCGCCCTCGCGCGCGCCAGCTTGAGGCGGCGCGCTGC 256  
QY 265 CCCGCGTCCCGGAGCGCGTGAAGCTGCGGAGGCGCATGAGCGCGCGCGCGCGAGCGGCGC 324  
DB CCCGCGTCCCGGAGCGCGTGAAGCTGCGGAGGCGCATGAGCGCGCGCGCGCGAGCGGCGC 316  
QY 325 GCTGAACGCTTGGGAGGCGCTGCGGAGGCGCATGCGGCGCGCGCGCGCGCGCGCTT 384  
DB GCTGAACGCTTGGGAGGCGCTGCGGAGGCGCATGCGGCGCGCGCGCGCGCGCGCGCTT 376  
QY 385 CTGCGAGGCTGAGACCGCGGCTGCGCGCGCGCGCATGAGGCGCGCTGATGCGCGAGCT 444  
DB CTGCGAGGCTGAGACCGCGGCTGCGCGCGCGCGCATGAGGCGCGCTGATGCGCGAGCT 436  
QY 445 GCTGGGCAACGCGCGTGTATGCTCGCTTGTGCGCGCATGAGGCTCGAGCGCGAGGAG 504  
DB GCTGGGCAACGCGCGTGTATGCTCGCTTGTGCGCGCATGAGGCTCGAGCGCGAGGAG 496  
QY 505 CAACCTTCTGCTGCTCAACCTGCGCATGCTGCGAGCTTGTGCGCGCTTGTGATGCC 564  
DB CAACCTTCTGCTGCTCAACCTGCGCATGCTGCGAGCTTGTGCGCGCTTGTGATGCC 556  
QY 565 ACTGATATGACCTTATGCTGCTGACAGCGCGCTGAGACCTTGGCGGCGCGCTGCAAGCT 624  
DB ACTGATATGACCTTATGCTGCTGACAGCGCGCTGAGACCTTGGCGGCGCGCTGCAAGCT 616  
QY 625 GTGGCTGTAGTGAATCACTGCTGCGACCTTCTGCTTCAACATGCTGCTCATCAG 684  
DB GTGGCTGTAGTGAATCACTGCTGCGACCTTCTGCTTCAACATGCTGCTCATCAG 676  
QY 685 CTACGACCGCTTCTGCTGCTGATACCGGAGCGGCTTCAACCGGCGCCAGAGGGTGAAC 744  
DB CTACGACCGCTTCTGCTGCTGATACCGGAGCGGCTTCAACCGGCGCCAGAGGGTGAAC 736  
QY 745 GCGGCGGAGAGTGGGAAATGCTGCTGCTGCTGCTGCTGCTTCTTCTGTAAGGAGC 804  
DB GCGGCGGAGAGTGGGAAATGCTGCTGCTGCTGCTGCTGCTTCTTCTGTAAGGAGC 796  
QY 805 AGGCATCTGAGCTGAGGAGTACCTGTCGAGGAGGAGCTGCATCCCGAGGAGCACTGCTA 864  
DB AGGCATCTGAGCTGAGGAGTACCTGTCGAGGAGGAGCTGCATCCCGAGGAGCACTGCTA 856  
QY 865 TGGCGAGTCTTCTACATGTAATCTTCTCATCAAGGCTTCCACCGCTGAGTCTTTTAC 924  
DB TGGCGAGTCTTCTACATGTAATCTTCTCATCAAGGCTTCCACCGCTGAGTCTTTTAC 916  
QY 925 GCGCTTCTCAGGCTTCACTTTTAACTTCAAGCATCTCAAGATCAATCAAGAGGCGCAC 964  
DB GCGCTTCTCAGGCTTCACTTTTAACTTCAAGCATCTCAAGATCAATCAAGAGGCGCAC 976  
QY 985 CCGGCTCCGAGTATGAGGCTGAGAGGAGCGGCGCGGAGCGGCTTCCGAGGCGCA 1044



Db 977 CCGCCTCCGCGCTGGATGGGGCTTCGAGAGGCGACCGGAGCCGCCCTTCCGAGGCCCA 1036  
QY 1045 GCCCTCAACCAACCCCAACCCGCTGGCTGGCTGGGGCTGCTGGCAGAGAGGGGACCGGGAGGC 1104  
Db 1037 GCCCTCAACCAACCCCAACCCGCTGGCTGGCTGGGGCTGCTGGCAGAGAGGGGACCGGGAGGC 1096  
QY 1105 CATGCCGCTGCAACAGATGGGGTGGGTGAGGCGGCGTGAAGCGCTGAAGCGCGGGAGGC 1164  
Db 1097 CATGCCGCTGCAACAGATGGGGTGGGTGAGGCGGCGTGAAGCGCTGAAGCGCGGGAGGC 1156  
QY 1165 GACCCCTCGGGGGGTGGGGGTGGGGCGGCTCCGTGGCTTCAACCCACTCCAGCTCCGGCAG 1224  
Db 1157 GACCCCTCGGGGGGTGGGGGTGGGGCGGCTCCGTGGCTTCAACCCACTCCAGCTCCGGCAG 1216  
QY 1225 CTCCTCGAGGGGACTGAGAGGCGCGCTCACTCAAGAGGGGCTCCAGCGCGTGGCGTC 1284  
Db 1217 CTCCTCGAGGGGACTGAGAGGCGCGCTCACTCAAGAGGGGCTCCAGCGCGTGGCGTC 1276  
QY 1285 CTCGGCCTCGTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTGCACCGCGCTTTG 1344  
Db 1277 CTCGGCCTCACTGAGAGAGCGCATGAAGATGGTGTCCAGAGCTTGCACCGCGCTTTG 1336  
QY 1345 GCTGTCTCGGGACAGAGAAAGTGGCCAAATGCTGGCGCTCATATGGAGCATCTTTGGGCT 1404  
Db 1337 GCTGTCTCGGGACAGAGAAAGTGGCCAAATGCTGGCGCTCATATGGAGCATCTTTGGGCT 1396  
QY 1405 CTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGCGCATGGCAGCTGCGT 1464  
Db 1397 CTGCTGGGCCCCATACACGCTGCTGATGATCATCCGGGCGCGCTGCGCATGGCAGCTGCGT 1456  
QY 1465 CCCTGACTACTGATGAGAAACCTCTTCTGGGCTCTGTGGGCGCAACTGGGCTGTCAACC 1524  
Db 1457 CCCTGACTACTGATGAGAAACCTCTTCTGGGCTCTGTGGGCGCAACTGGGCTGTCAACC 1516  
QY 1525 TGTTCCTTACCTCTGTGTCACCAAGAGCTTCCGGGCGGCTTCAACCAAGCTGTGCGCC 1584  
Db 1517 TGTTCCTTACCTCTGTGTCACCAAGAGCTTCCGGGCGGCTTCAACCAAGCTGTGCGCC 1576  
QY 1585 CCAGAGCTCAAAATTCAGACCCCAACAGCTCCCTGAGACATGCTGAGAAATGATGGGCCA 1644  
Db 1577 CCAGAGCTCAAAATTCAGACCCCAACAGCTCCCTGAGACATGCTGAGAAATGATGGGCCA 1636  
QY 1645 CCAGAGCTTCCCTCAGCCACGCTCTCTGAGCCAGGCTCTCTGGGCAATGGGCGCTGCT 1704  
Db 1637 CCAGAGCTTCCCTCAGCCACGCTCTCTGAGCCAGGCTCTCTGGGCAATGGGCGCTGCT 1696  
QY 1705 GCGCCCTACCGGCTGCTTCCCGCAGGGGTGAGCCCGCGTGTCTGTGGCCCTCTCTTA 1764  
Db 1697 GCGCCCTACCGGCTGCTTCCCGCAGGGGTGAGCCCGCGTGTCTGTGGCCCTCTCTTA 1756  
QY 1765 ATGCCACGGCAGCACCCTGCAATGAGGCGGCTTCTGGGTTGGCCAGAGGGCCCTCA 1824  
Db 1757 ATGCCACGGCAGCACCCTGCAATGAGGCGGCTTCTGGGTTGGCCAGAGGGCCCTCA 1816  
QY 1825 CTGGCTGACTGAGGCTGGGTGGGCGGCTTCCCGCACAATTCTGGCTCAACCGGGGA 1884  
Db 1817 CTGGCTGACTGAGGCTGGGTGGGCGGCTTCCCGCACAATTCTGGCTCAACCGGGGA 1875  
QY 1885 GGGACAGTGTGAGAGTCCAGACATCTGCCCCACCCCTGCTGGTCCCAACCTTGGCAG 1944  
Db 1876 GGGACAGTGTGAGAGTCCAGACATCTGCCCCACCCCTGCTGGTCCCAACCTTGGCAG 1935  
QY 1945 TTAGTGTGTGTGTCTTCCAAAGACACCTGGGTGTGCTCAGAGGCTCTCTGCGCTA 2004  
Db 1936 TTAGTGTGTGTGTCTTCCAAAGACACCTGGGTGTGCTCAGAGGCTCTCTGCGCTA 1995  
QY 2005 GAGATTGTGCTTGTGACATGACACCTGTGACACCTGTGACACACCTGTGACACCGTCC 2064  
Db 1996 GAGATTGTGCTTGTGACATGACACCTGTGACACCTGTGACACACCTGTGACACCGTCC 2055  
QY 2065 CTCTCCCGGAGAACGCCAGACATGCTTTGCTGCTTGTCTCTTGGCATTAAGCTTC 2124  
Db 2056 CTCTCCCGGAGAACGCCAGACATGCTTTGCTGCTTGTCTCTTGGCATTAAGCTTC 2115

QY 2125 AGGCTGAGCCCTTTCACACCCCTTCCCAACACTCTCTGCCCCCAAAAGTCAAGG 2184  
Db 2116 AGGCTGAGCCCTTTCACACCCCTTCCCAACACTCTCTGCCCCCAAAAGTCAAGG 2175  
QY 2185 GCCCTAGAACTCGAAGCTGTTCTCTGCTTTCCATTCTGGGTGTTTTCAAGATGA 2244  
Db 2176 GCCCTAGAACTCGAAGCTGTTCTCTGCTTTCCATTCTGGGTGTTTTCAAGATGA 2235  
QY 2245 AGAAGAAACATGCTGTGAATGATGTTGCGGGATGTTTAATCAAGAGACAAAT 2304  
Db 2236 AGAAGAAACATGCTGTGAATGATGTTGCGGGATGTTTAATCAAGAGACAAAT 2295  
QY 2305 TGGTGAAGACTCAGGAGCTGATTGGCAGATGGGCTGCCAGGCCCTCTCCCTCGCT 2364  
Db 2296 TGGTGAAGACTCAGGAGCTGATTGGCAGATGGGCTGCCAGGCCCTCTCCCTCGCT 2355  
QY 2365 AAGGCTTCCGCTGAGCTGTGCAGCTGCTTGTGCCACCCGCGCTTGGGCTCACCA 2424  
Db 2356 AAGGCTTCCGCTGAGCTGTGCAGCTGCTTGTGCCACCCGCGCTTGGGCTCACCA 2415  
QY 2425 GCGCTGTGGCCAGCGCTGCGCGGCACTGTTGTGCTCACCGAGACCTGCGGGGTT 2484  
Db 2416 GCGCTGTGGCCAGCGCTGCGCGGCACTGTTGTGCTCACCGAGACCTTGGGGTT 2475  
QY 2485 GTTGGAGAGAGGGGCGCGGCTGGGCGCGAGGGTCCAAAGCGTGCAGGGGCGTTCAGA 2544  
Db 2476 GTTGGAGAGAGGGGCGCGGCTGGGCGCGAGGGTCCAAAGCGTGCAGGGGCGTTCAGA 2535  
QY 2545 GGAAGTGTCCCGGCGAGGGGCGGCTTGCATGTGCTGTGACACCGGCTCAACCGCGCTTGC 2604  
Db 2536 GGAAGTGTCCCGGCGAGGGGCGGCTTGCATGTGCTGTGACACCGGCTCAACCGCGCTTGC 2595  
QY 2605 ATGTCTCTGTGCTGTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 2664  
Db 2596 ATGTCTCTGTGCTGTGCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 2655  
QY 2665 ATTTTAAAAA 2688  
Db 2656 ATTTTAAAAA 2679  
  
RESULT 11  
AAH44572  
ID AAH44572 standard; cDNA; 2689 BP.  
XX  
AC AAH44572;  
DT 20-MAR-2003 (revised)  
DT 01-NOV-2001 (first entry)  
XX  
DE Human muscarinic acetylcholine receptor 6 encoding cDNA seq ID NO:1.  
XX  
KW Human; muscarinic acetylcholine receptor 6; mAChR-6; detection;  
KW antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidiabetic;  
KW antidepressant; antirhythmic; antiinflammatory; cartiline; pain;  
KW G-protein coupled receptor; nervous system related disorder; xerostomia;  
KW disorders affecting consciousness; affective disorder; movement disorder;  
KW irritable bowel syndrome; drinking disorder; gland related disorder;  
KW smooth muscle related disorder; cardiac muscle disorder; eating disorder;  
KW diabetes mellitus; diagnosis; drug screening; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 291..1628  
FT /\*tag= a  
FT /product= "muscarinic acetylcholine receptor 6"  
PN US6093545-A.  
XX  
PD 25-JUL-2000.  
XX



|||||  
1577 CCAGAGCTCAAAATCCAGCCACACAGCTCCCTGGAGCACTGCTGGAAGTGAAGTGCCCA 1636  
|||||  
1645 CCAGAGCTCCCTCAGCCACAGCTCTCTCAGCCAGAGTCTCTGGGCATCTGGCCCTGCT 1704  
|||||  
1637 CCAGAGCTCCCTCAGCCACAGCTCTCTCAGCCAGAGTCTCTGGGCATCTGGCCCTGCT 1696  
|||||  
1705 GCCCCCTACCCGGCTGTTCCGCCAGGGGTGAGCCCGCGTGTCTGTGGCCCTCTCTTA 1764  
|||||  
1697 GCCCCCTACCCGGCTGTTCCGCCAGGGGTGAGCCCGCGTGTCTGTGGCCCTCTCTTA 1756  
|||||  
1765 ATGCCACGCGACGACCTCCCATGGAGCGGCTTCTCTGGGTGGCCAGAGGCGCCCTCA 1824  
|||||  
1757 ATGCCACGCGACGACCTCCCATGGAGCGGCTTCTCTGGGTGGCCAGAGGCGCCCTCA 1816  
|||||  
1825 CTGGCTGGAATGAGGCTGGGTGGCGCCCTGCGCCCAATCTCTGGCTCACCAGGGA 1884  
|||||  
1817 CTGGCTGGAATGAGGCTGGGTGGCGCCCTGCGCCCAATCTCTGGCTCACCAGGGA 1875  
|||||  
1885 GGGACAGTCTGGAGTCCGAGCATGCTGCCACCCCTGCTGGTGGCCACCCCTTCGCG 1944  
|||||  
1876 GGGACAGTCTGGAGTCCGAGCATGCTGCCACCCCTGCTGGTGGCCACCCCTTCGCG 1935  
|||||  
1945 TTACTGTTGGTGTCTTCCCAAGCAAGCACTGGGTGCTGCTCAAGGCTTCTTGCCTTA 2004  
|||||  
1936 TTACTGTTGGTGTCTTCCCAAGCAAGCACTGGGTGCTGCTCAAGGCTTCTTGCCTTA 1995  
|||||  
2005 GGAGTTTGGCTTGACGTCGACACACCTGCAACCCCTGCAACACCTGCAACCCGTC 2064  
|||||  
1996 GCAGTTTGGCTTGACGTCGACACACCTGCAACCCCTGCAACACCTGCAACCCGTC 2055  
|||||  
2065 CTCTCCCGGACAGCCGAGGACACCTGCTTGTGCTTGTGCTTGTCTTGTGATAGCTC 2124  
|||||  
2056 CTCTCCCGGACAGCCGAGGACACCTGCTTGTGCTTGTGCTTGTCTTGTGATAGCTC 2115  
|||||  
2125 AGGCTTGGGCTTTCACCCCTCTTCCCAACAACTCTCTGCGCCCAAGTGTCAAGG 2184  
|||||  
2116 AGGCTTGGGCTTTCACCCCTCTTCCCAACAACTCTCTGCGCCCAAGTGTCAAGG 2175  
|||||  
2185 GGCCTAGGAACCTCGAAGCTGTCTGCTTTTCAATCTGGGTGTTTCAAGAGATGA 2244  
|||||  
2176 GGCCTAGGAACCTCGAAGCTGTCTGCTTTTCAATCTGGGTGTTTCAAGAGATGA 2235  
|||||  
2245 AGAAGAAACATGCTGTGAATGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2304  
|||||  
2236 AGAAGAAACATGCTGTGAATGATGCTGATGCTGATGCTGATGCTGATGCTGATG 2295  
|||||  
2305 TGCTAGGAGCTCAGGCTGAGTTGGAGGTGGGCTCCACGCGCTCTCTCCCTCCGCT 2364  
|||||  
2296 TGCTAGGAGCTCAGGCTGAGTTGGAGGTGGGCTCCACGCGCTCTCTCCCTCCGCT 2355  
|||||  
2365 AAGGCTTCGGGTGAGCTGTCAGCTGTTCTGCGCCACCCGCTCTGGGCTCACACA 2424  
|||||  
2356 AAGGCTTCGGGTGAGCTGTCAGCTGTTCTGCGCCACCCGCTCTGGGCTCACACA 2415  
|||||  
2425 GGCCTGGTGGCAAGCTTCCCGGCACTGTTGCTTCCACCCAGGACCTCTGGGGTT 2484  
|||||  
2416 GGCCTGGTGGCAAGCTTCCCGGCACTGTTGCTTCCACCCAGGACCTCTGGGGTT 2475  
|||||  
2485 GTTGGAGAGGGGGCGGCTGGGCTCCAGGGTCCAGGGGTGAGGGGGGCTCCAGA 2544  
|||||  
2476 GTTGGAGAGGGGGCGGCTGGGCTCCAGGGTCCAGGGGTGAGGGGGGCTCCAGA 2535  
|||||  
2545 GGAGTGGCCCGGAGGGCCGCTTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2604  
|||||  
2536 GGAGTGGCCCGGAGGGCGGCTTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2595  
|||||  
2605 ATGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2664  
|||||  
2596 ATGCTCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2655  
|||||  
2665 ATTTTTTTAAAAA 2688  
|||||

Db 2656 ATTTTTTTAAAAA 2679

RESULT 12  
ABX11852  
ID ABX11852 standard; cDNA; 2689 BP.  
XX  
AC ABX11852;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Human cDNA encoding muscarinic acetylcholine receptor 6, mAChR-6.  
XX  
KW Human; ss; gene; mAChR-6; muscarinic acetylcholine receptor-6;  
KW cognitive disorder; amnesia; amnesic spatial disorientation;  
KW Klüver-Bucy syndrome; Alzheimer's related memory loss;  
KW learning disability; consciousness disorder; visual hallucination;  
KW delirium; schizo-effective disorder; schizophrenia; depression;  
KW affective disorder; sleep disorders; pain generation disorder;  
KW irritable bowel syndrome; chest pain; movement disorder;  
KW Parkinson's disease; eating disorder; insulin hypersecretion obesity;  
KW heart muscle disorder; bradycardia; tachycardia; flutter;  
KW fibrillation; gland related disorder; xerostomia; diabetes mellitus.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 291..1628  
FT /\*tag= a  
FT /product= "mAChR-6"  
XX  
PN US2002166131-A1.  
XX  
PD 07-NOV-2002.  
XX  
PF 08-JUL-1999; 99US-00349755.  
XX  
PR 04-DEC-1997; 97US-00985090.  
XX  
PR 17-MAR-1998; 98US-00042780.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
PI Goodearl ADJ, Glucksmann MA;  
XX  
DR WPI; 2003-298709/29.  
DR P-PSDB; ABG76405.  
XX  
CC New muscarinic acetylcholine receptor 6 (mAChR-6) nucleic acids and  
PT proteins, useful for modulating acetylcholine or phosphatidylinositol,  
PT particularly for treating e.g. schizophrenia, chest pain, tachycardia or  
PT arrhythmia.  
XX  
PS Claim 7; Fig 1; 66pp; English.  
XX  
CC The invention relates to an isolated human or rat muscarinic  
CC acetylcholine receptor 6 (mAChR-6) nucleic acid molecule and the encoded  
CC protein. Also included are (non-human) host cells comprising the mAChR-6  
CC nucleic acid molecule, an antibody that selectively binds the polypeptide  
CC above, a method for producing the polypeptide by culturing the host cell  
CC such that the mAChR-6 nucleic acid is expressed, a method for detecting  
CC the presence of the mAChR-6 polypeptide and nucleic acid, a method for  
CC identifying a compound that binds to the mAChR-6 polypeptide and a method  
CC for modulating the activity of the mAChR-6 polypeptide. The mAChR-6  
CC polynucleotide, polypeptide, antibody or modulator are useful in drug  
CC screening assays, diagnostic assays for identifying diseases, allelic  
CC screening, pharmacogenetic testing, methods of treatment,  
CC pharmacogenomics or monitoring the effects during clinical trials. In  
CC particular, the mAChR-6 polynucleotide, polypeptide or antibody is useful  
CC for treating or diagnosing cognitive disorders (e.g. amnesia, amnesic  
CC spatial disorientation, Klüver-Bucy syndrome, Alzheimer's related memory  
CC loss or learning disability), disorders affecting consciousness (e.g.  
CC visual hallucinations or delirium), schizo-effective disorders (e.g.  
CC schizophrenia or depression), affective disorders (e.g. sleep disorders),

CC	disorders affecting pain generation mechanisms (e.g. pain related to
CC	irritable bowel syndrome, or chest pain), movement disorders (e.g.
CC	Parkinson's disease), eating disorders (e.g. insulin hypersecretion
CC	obesity), heart muscle related disorders (e.g. bradycardia, tachycardia,
CC	arrhythmia, flutter or fibrillation), or gland related disorder (e.g.
CC	xerostomia or diabetes mellitus). The present sequence encodes human
XX	MAHR-6
SQ	Sequence 2689 BP; 393 A; 990 C; 806 G; 500 T; 0 U; 0 Other;
Query Match 97.6%; Score 2635.2; DB 8; Length 2689;	
Best Local Similarity 99.8%; Pred. No. 0;	
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;	
QY	25 CGACCGGAGCGGCTCAGGCTCCGGCTCTCTCCGGCTGCAGCAGCGCGTGC CGGC 84
DB	18 CGACCGGAGCGGCTCAGGCTCCGGCTCTCTCCGGCTGCAGCAGCGCGTGC CGGC 77
QY	85 CCACCTGGGCTCGGATCCGGCCCGGCCCCCTCGGGCAACCGCTGTGCGCCCGGCCG 144
DB	78 CCACCTGGGCTCGGATCCGGCCCGGCCCCCTCGGGCAACCGCTGTGCGCCCGGCCG 137
QY	145 GCCCGCGGACCATGGCTGGGCGCCCCCAGAGGGAAACCGCCGCAAGGGCCCGCA 204
DB	138 GCCCGCGGACCATGGCTGGGCGCCCCCAGAGGG- AACC CGACCCCGGCCAAGGGCCCGCA 196
QY	205 AAGACGAGGCTCCCGGGCGGGCCCCCTCCCGGCCCGCCAGCTCTCGGCGGGCCCTCG 264
DB	197 AAGACGAGGCTCCCGGGCGGGCCCCCTCCCGGCCCGCCAGCTCTCGGCGGGCCCTGC 256
QY	265 CCGCGTCCCGGAGCGCGTGAAGCTGTGGGGCATGAGAGCGCGCCCGCCGAGCGGGCC 324
DB	257 CCGCGTCCCGGAGCGCGTGAAGCTGTGGGGCATGAGAGCGCGCCCGCCGAGCGGGCC 316
QY	325 GCTGAACGCTTCGGGGCGCGTGGCGGCGATGGGGGGCGGGCGGGCGGGCGGCTT 384
DB	317 GCTGAACGCTTCGGGGCGCGTGGCGGCGAGCGGGCGGGCGGGCGGGCGGGCGGCTT 376
QY	385 CTCGGCAGGCTTGACCGCGGCTGGCGCGCTCATGGCGCTCATCGTGGCCACGCT 444
DB	377 CTCGGCAGGCTTGACCGCGGCTGGCGCGCTCATGGCGCTCATCGTGGCCACGCT 436
QY	445 GTGGGCAACGCGTGGTCACTCGCTTCGCTTCGTCGGCCGACTCGAGCTCCGACCCAGAA 504
DB	437 GCTGGCAACGCGTGGTCACTCGCTTCGCTTCGTCGGCCGACTCGAGCTCCGACCCAGAA 496
QY	505 CAACTTCTTCTCTCAACCTCGCATCTCCGACTTCTCGTCGGGGCTTCTGATCCC 564
DB	497 CAACTTCTTCTCTCAACCTCGCATCTCCGACTTCTCGTCGGGGCTTCTGATCCC 556
QY	565 ACTGTATGTACCTTACGCTGACAGGCGGCTGGACCTTCGCGCGGGGCTCTGCAAGCT 624
DB	557 ACTGTATGTACCTTACGCTGACAGGCGGCTGGACCTTCGCGCGGGGCTCTGCAAGCT 616
QY	625 GTGGCTGTGTGGACTACTCGTGTGACACTCTCTGCTTCAACATCGTCTCATCAG 684
DB	617 GTGGCTGTGTGGACTACTCGTGTGACACTCTCTGCTTCAACATCGTCTCATCAG 676
QY	685 CTACGACCGCTTCTCTCGGTCAACCGAGCGGTCTCATACCGGGCCAGCAGGGTGACAC 744
DB	677 CTACGACCGCTTCTCTCGGTCAACCGAGCGGTCTCATACCGGGCCAGCAGGGTGACAC 736
QY	745 GCGGGCGGCGAGTGGGAAGATGCTGTGTGTGGGTGGCTTCTGCTGTACGGACC 804
DB	737 GCGGGCGGCGAGTGGGAAGATGCTGTGTGTGGGTGGCTTCTGCTGTACGGACC 796
QY	805 AGCCATCTCTAGCTGGAGTACTGTCTGGGGGCGAGCTCCATCCCGAGGGCCACTGTCTA 864
DB	797 AGCCATCTCTAGCTGGAGTACTGTCTGGGGGCGAGCTCCATCCCGAGGGCCACTGTCTA 856
QY	865 TGCCAGGTTCTTCTACAACTGGTACTTCTCTCATCAGGGCTTCCACCTGGAGTTCTTTAC 924
DB	857 TGCCAGGTTCTTCTACAACTGGTACTTCTCTCATCAGGGCTTCCACCTGGAGTTCTTTAC 916

QY	925 GCCCTTCTCAGCGTCACCTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCAC 984
DB	917 GCCCTTCTCAGCGTCACCTTCTTTAACTCAGCATCTACCTGAACATCCAGAGGCGCAC 976
QY	985 CCGCTTCCGGCTGGATGGGGCTCGAGAGCAGCGGCCCCCGAGCCCTCTCCGAGGCCCCA 1044
DB	977 CCGCTTCCGGCTGGATGGGGCTCGAGAGCAGCGGCCCCCGAGCCCTCTCCGAGGCCCCA 1036
QY	1045 GCCCTCACCACCCACCGCTGGCTGGGGCTCTGGGAGAGGGGCAAGGGGAGGC 1104
DB	1037 GCCCTCACCACCCACCGCTGGCTGGGGCTCTGGGAGAGGGGCAAGGGGAGGC 1096
QY	1105 CATGCCGCTGCA CAGGTATGGGGTGGTGAGCGGCGCTGAGGCGCGGGAGGC 1164
DB	1097 CATGCCGCTGCA CAGGTATGGGGTGGTGAGCGGCGCTGAGGCGCGGGAGGC 1156
QY	1165 GACCTTCGGGGTGGCGGTGGGGGGGCTCCGTGGCTTACCCACCTCAGACTCCGGCAG 1224
DB	1157 GACCTTCGGGGTGGCGGTGGGGGGGCTCCGTGGCTTACCCACCTCAGACTCCGGCAG 1216
QY	1225 CTCCTCGAGGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTCCAAGCGTCGCGCTC 1284
DB	1217 CTCCTCGAGGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTCCAAGCGTCGCGCTC 1276
QY	1285 CTCGCTCTGCTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCCACCAGCGCTTTCG 1344
DB	1277 CTCGCTCTGCTGGAGAGCGCATGAAGATGGTGTCCAGAGCTTCCACCAGCGCTTTCG 1336
QY	1345 GCTGTCTGGGACAGGAAAGTGGCCAAAGTGGCTGGCGCTCATCTGAGAGCATCTTTGGGCT 1404
DB	1337 GCTGTCTGGGACAGGAAAGTGGCCAAAGTGGCTGGCGCTCATCTGAGAGCATCTTTGGGCT 1396
QY	1405 CTGCTGGGCCCCATACAGCTCTGATGATCATCGGGCGGCTGCATCGGCGCACCTGCT 1464
DB	1397 CTGCTGGGCCCCATACAGCTCTGATGATCATCGGGCGGCTGCATCGGCGCACCTGCT 1456
QY	1465 CCCTGACTACTGGTACGAAACCTCTTCTGGGTCTCTGGGGCCAACTCGGCTGTCAACCC 1524
DB	1457 CCCTGACTACTGGTACGAAACCTCTTCTGGGTCTCTGGGGCCAACTCGGCTGTCAACCC 1516
QY	1525 TGTCTCTACCTCTGTGTCACACAGCTTCGCGCGGGCTTCAACAGCTGTCTGCCC 1584
DB	1517 TGTCTCTACCTCTGTGTCACACAGCTTCGCGCGGGCTTCAACAGCTGTCTGCCC 1576
QY	1585 CCAGAGCTCAAAATCCAGCCCCCAGCTCCCTGGAGCACTGCTGGAAGTGAAGTGGCCCCA 1644
DB	1577 CCAGAGCTCAAAATCCAGCCCCCAGCTCCCTGGAGCACTGCTGGAAGTGAAGTGGCCCCA 1636
QY	1645 CCAGAGCTTCCCTCAGCCACGCTCTCTCAGCCCCAGGTCTCTGGGCACTCTGGCCCTGCT 1704
DB	1637 CCAGAGCTTCCCTCAGCCACGCTCTCTCAGCCCCAGGTCTCTCTGGGCACTCTGGCCCTGCT 1696
QY	1705 GCGCCCTACCGGCTCGTTTCCCGCAGGGGTAGCCCCCGCGTGTGTGTGGCCCTCTCTTA 1764
DB	1697 GCGCCCTACCGGCTCGTTTCCCGCAGGGGTAGCCCCCGCGTGTGTGTGGCCCTCTCTTA 1756
QY	1765 ATGCCACGCGACCGCTGCCATGAGGCGCTTCTCTGGGTGGCCAGAGGCCCCCTCA 1824
DB	1757 ATGCCACGCGACCGCTGCCATGAGGCGCTTCTCTGGGTGGCCAGAGGCCCCCTCA 1816
QY	1825 CTGGCTGGAAGTGGGGTGGCGGCTTGGCCCCCCCCCACAATTCTGGGTCTCACCGGGGA 1884
DB	1817 CTGGCTGGAAGTGGGGTGGCGGCTTGGCCCCCCCCCACAATTCTGGGTCTCACCG- GGGA 1875
QY	1885 GGGACAGCTGTGAGGTCCAGACATGTGTCACACCCCTGTGTGTGGTCCCACTTCGCGAG 1944
DB	1876 GGGACAGCTGTGAGGTCCAGACATGTGTCACACCCCTGTGTGTGGTCCCACTTCGCGAG 1935
QY	1945 TTACTGGTGTGTGTTCTTCCCAAGCAACCTGGGTGTGCTCCAGGCTTCTTGGCCCTA 2004
DB	1936 TTACTGGTGTGTGTTCTTCCCAAGCAACCTGGGTGTGCTCCAGGCTTCTTGGCCCTA 1995



QY	481	CGACTCGAGCCTCCGCAACCCAGAAACAACTTCTCTGCTCAACCTCGCCATCTCCGACTT	540
Db	481	CGACTCGAGCCTCCGCAACCCAGAAACAACTTCTCTGCTCAACCTCGCCATCTCCGACTT	540
QY	541	CCTCGTCGGGCGCTTCTGCAATCCCACTGATGTAACCTTACCTGCTGACAGGCGGCTGGAC	600
Db	541	CCTCGTCGGGCGCTTCTGCAATCCCACTGATGTAACCTTACCTGCTGACAGGCGGCTGGAC	600
QY	601	CTTTCGGCGCGGCTTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACACCTCTTC	660
Db	601	CTTTCGGCGCGGCTTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACACCTCTTC	660
QY	661	TGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGCTCGGTCAACCGAGCGGTCTC	720
Db	661	TGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGCTCGGTCAACCGAGCGGTCTC	720
QY	721	ATACCGGGCCGACAGGGGTGACACGGGGGGGAGTGGGAAGATGCTGCTGGTGGGT	780
Db	721	ATACCGGGCCGACAGGGGTGACACGGGGGGGAGTGGGAAGATGCTGCTGGTGGGT	780
QY	781	GCTGCGCTTCTGCTGTACGGACACAGCCATCTGAGCTGGGAGTACCTGTCCGGGGGAG	840
Db	781	GCTGCGCTTCTGCTGTACGGACACAGCCATCTGAGCTGGGAGTACCTGTCCGGGGGAG	840
QY	841	CTCCATCCCGAGGGCCACTGCTATGCCAGTTCCTTCTAACATGCTGCTCTCTCATCAC	900
Db	841	CTCCATCCCGAGGGCCACTGCTATGCCAGTTCCTTCTAACATGCTGCTCTCTCATCAC	900
QY	901	GGCTTCCACCTGGAGTTCCTTAAACCTTCTCAGCGTACCTTCTTAACTCAGCAT	960
Db	901	GGCTTCCACCTGGAGTTCCTTAAACCTTCTCAGCGTACCTTCTTAACTCAGCAT	960
QY	961	CTACCTGAACATCCAGAGCGCACCGCTCCGGCTGGATGGGCTCGAGAGCGACCGG	1020
Db	961	CTACCTGAACATCCAGAGCGCACCGCTCCGGCTGGATGGGCTCGAGAGCGACCGG	1020
QY	1021	CCCGAGCGCTTCCGAGGGCCAGCCCTCACACCCCGCCCTGCTGCTGGGGCTG	1080
Db	1021	CCCGAGCGCTTCCGAGGGCCAGCCCTCACACCCCGCCCTGCTGCTGGGGCTG	1080
QY	1081	CTGGAGAGAGGGGACAGGGGAGGCAATGCCGTGACACAGGTATGGGGTGGGTGAGCGGC	1140
Db	1081	CTGGAGAGAGGGGACAGGGGAGGCAATGCCGTGACACAGGTATGGGGTGGGTGAGCGGC	1140
QY	1141	CGTAGGCGCTGAGGCGGGGGAGGCAACCTTCGGGGGTGGCGGTGGGGCGGCTCCGTGGC	1200
Db	1141	CGTAGGCGCTGAGGCGGGGGAGGCAACCTTCGGGGGTGGCGGTGGGGCGGCTCCGTGGC	1200
QY	1201	TTTACCCACCTCCAGCTCCGGCAGCTTCTCGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
Db	1201	TTTACCCACCTCCAGCTCCGGCAGCTTCTCGAGGGGCACTGAGAGGCGCGCTCACTCAA	1260
QY	1261	GAGGGGCTCAAAGCGCTCGGCGTCTCGGCTGCTGAGAGAGCGCATGAAGTGGTGTG	1320
Db	1261	GAGGGGCTCAAAGCGCTCGGCGTCTCGGCTGCTGAGAGAGCGCATGAAGTGGTGTG	1320
QY	1321	CGAGAGCTTCAACCGAGCTTTCGGCTGTCTC- GGGACAGGAAGTGGCCAGTGCCTGG	1379
Db	1321	CGAGAGCTTCAACCGAGCTTTCGGCTGTCTC- GGGACAGGAAGTGGCCAGTGCCTGG	1380
QY	1380	CGGTATCTGAGCATCTTTTGGGCTTCTGCTGGGCGCCATACACGCTGCTGATGATCATCC	1439
Db	1381	CGGTATCTGAGCATCTTTTGGGCTTCTGCTGGGCGCCATACACGCTGCTGATGATCATCC	1440
QY	1440	GGGCGGCTGCAAGGCACTGCGTCCCTGACTACTGGTACGAACCTCTCTGGCTCC	1499
Db	1441	GGGCGGCTGCAAGGCACTGCGTCCCTGACTACTGGTACGAACCTCTCTGGCTCC	1500
QY	1500	TGTGGGCGCACTCGGCTGTCAACCTCTCTTACCTCTGTGCCACCACTTCCGCG	1559
Db	1501	TGTGGGCGCACTCGGCTGTCAACCTCTCTTACCTCTGTGCCACCACTTCCGCG	1560

RESULT 14

AAS62391

ID AAS62391 standard; cDNA; 2173 BP.

XX

QY	1560	GGGCGCTTCAACAGCTGTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGCTCCCTGG	1619
Db	1561	GGGCGCTTCAACAGCTGTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGCTCCCTGG	1620
QY	1620	AGCACTGCTGGAAGTGAAGTGGCCACCAAGAGCTCCCTCAGCCACGCTCTCTCAGCCCA	1679
Db	1621	AGCACTGCTGGAAGTGAAGTGGCCACCAAGAGCTCCCTCAGCCACGCTCTCTCAGCCCA	1680
QY	1680	GGTCTCTCTGGGCAATCTGGGCCCTGCTGCCCTTACCCGGCTCGTTCCCTCCAGGGGTGAGCC	1739
Db	1681	GGTCTCTCTGGGCAATCTGGGCCCTGCTGCCCTTACCCGGCTCGTTCCCTCCAGGGGTGAGCC	1740
QY	1740	CGGCGGTGTCTGTGGCCCTCTCTTAATGCCACGGAGCACCCCTGTCATATGAGGGGCTT	1799
Db	1741	CGGCGGTGTCTGTGGCCCTCTCTTAATGCCACGGAGCACCCCTGTCATATGAGGGGCTT	1800
QY	1800	CCTGGGTTGGCCAGAGGGGCCCTCACTGGCTGGACTGGAGGCTGGGTGGCGGCCCTGCC	1859
Db	1801	CCTGGGTTGGCCAGAGGGGCCCTCACTGGCTGGACTGGAGGCTGGGTGGCGGCCCTGCC	1860
QY	1860	CCCCACATTTCTGGCTCCACCGGGAGGGACAGTCTGGAGGTCCTCAGACATGCTGCCACAC	1919
Db	1861	CCCCACATTTCTGGCTCCACCGGGAGGGACAGTCTGGAGGTCCTCAGACATGCTGCCACAC	1920
QY	1920	CCCTGCTGTGTCGCCACCTTTCGAGTTACTGTTGGTGTCTTCCCAAAGACGACCTG	1979
Db	1921	CCCTGCTGTGTCGCCACCTTTCGAGTTACTGTTGGTGTCTTCCCAAAGACGACCTG	1980
QY	1980	GGTGTGCTCCAGGCTTCTGCGCTAGCAGTTTGGCTCTGCAGTGCACACCTGCACAC	2039
Db	1981	GGTGTGCTCCAGGCTTCTGCGCTAGCAGTTTGGCTCTGCAGTGCACACCTGCACAC	2040
QY	2040	CCCTGCACACACTGCACACCGCTCCTCCTCCCGGACAAAGCCAGGACACTGCTTTTGT	2099
Db	2041	CCCTGCACACACTGCACACCGCTCCTCCTCCCGGACAAAGCCAGGACACTGCTTTTGT	2100
QY	2100	GCCTTCTGTCTTGCATAAGCTCAGGCTCGGCTTTTCCACCTCTTCCCAACCAATC	2159
Db	2101	GCCTTCTGTCTTGCATAAGCTCAGGCTCGGCTTTTCCACCTCTTCCCAACCAATC	2160
QY	2160	TCTCTGCCCGCCAAAAGTGTCAAGGGGCGCTAGGAACTCGAAGCTTCTTCTGCTTTTCC	2219
Db	2161	TCTCTGCCCGCCAAAAGTGTCAAGGGGCGCTAGGAACTCGAAGCTTCTTCTGCTTTTCC	2220
QY	2220	ATTCTGGGTGTTTTCAGAAAAGATGAAGAAAAATGCTGTGAATTTGATGTTCTGTTGG	2279
Db	2221	ATTCTGGGTGTTTTCAGAAAAGATGAAGAAAAATGCTGTGAATTTGATGTTCTGTTGG	2280
QY	2280	GATGTTTAAATCAAGAGAGACAAAATTTGCTGAGGAGCTCAGGGCTGGATTTGGCAGGTGTG	2339
Db	2281	GATGTTTAAATCAAGAGAGACAAAATTTGCTGAGGAGCTCAGGGCTGGATTTGGCAGGTGTG	2340
QY	2340	GCTCCACGCGCTCTCCTCCGCTAAGGCTTCCGGCTGAGCTGTGCCAGCTGCTTCTGC	2399
Db	2341	GCTCCACGCGCTCTCCTCCGCTAAGGCTTCCGGCTGAGCTGTGCCAGCTGCTTCTGC	2400
QY	2400	CCACCCCGCTCTGCGCTCACACAGCCCTGTGTGCGCAAGCCTGCCCGGCCACTCTGTT	2459
Db	2401	CCACCCCGCTCTGCGCTCACACAGCCCTGTGTGCGCAAGCCTGCCCGGCCACTCTGTT	2460
QY	2460	TGCTCACCCAGGACCTCTGGGGTTTGGGAGGAGGGGGCGGCTGGCGCCGAGGGTC	2519
Db	2461	TGCTCACCCAGGACCTCTGGGGTTTGGGAGGAGGGGGCGGCTGGCGCCGAGGGTC	2520
QY	2520	CCAAGCGGTGCAAGGGCGGTCCAGAGAGGTGCCCGGGCAGGGGCGCTTCCGCAT	2575
Db	2521	CCAAGCGGTGCAAGGGCGGTCCAGAGAGGTGCCCGGGCAGGGGCGCTTCCGCAT	2576

AC AAS62391;  
XX  
DT 14-FEB-2002 (first entry)  
XX  
DE cDNA sequence #178 encoding novel human secreted protein.  
XX  
KW Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KW immune deficiency disorder; blood disorder; inflammatory disorder;  
KW infectious disorder; gene therapy; antimicrobial; hepatotropic;  
KW immunosuppressive; antirheumatic; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO200177291-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 29-MAR-2001; 2001WO-US010485.  
XX  
XX 06-APR-2000; 2000US-0195604P.  
XX  
XX (GENY ) GENETICS INST INC.  
XX  
XX Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
PI Gulukota K, Graham JR;  
XX  
XX WPI; 2002-010900/01.  
XX  
XX New polynucleotides encoding secreted proteins useful for treating e.g.  
PT asthma, HIV and Crohn's disease.  
PT  
XX  
XX Claim 1; Page 168; 391pp; English.  
XX  
XX The present invention relates to the isolation of novel cDNA sequences  
CC which encode human secreted proteins. The cDNA sequences have been  
CC derived from a variety of human tissues. The invention also provides a  
CC method for producing proteins from these polynucleotide sequences. The  
CC proteins are useful for identifying compounds that modulate their  
CC activity and production, and the cell is also useful for identifying  
CC compounds that modulate expression of the polynucleotide sequences  
CC encoding the secreted proteins. The sequences of the invention are useful  
CC for treating diseases such as hyperproliferative disorders (e.g. cancer),  
CC immune deficiency disorders (e.g. severe combined immunodeficiency  
CC (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders  
CC (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and  
CC infectious disorders (e.g. hepatitis). The polynucleotide sequences of  
CC the invention are also useful in gene therapy. AAS62214-AAS62838  
CC represent the cDNA sequences of the invention that encode for novel human  
CC secreted proteins  
XX  
XX Sequence 2173 BP; 330 A; 772 C; 620 G; 451 T; 0 U; 0 Other;  
SQ  
Query Match 79.6%; Score 2149.2; DB 6; Length 2173;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2162; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
QY 508 CTTCTTCTGCTCAACCTCGCCATCTCGACTTCTCTGTCGGCGCTTCTGATCCCACT 567  
DB 1 CTTCTTCTGCTCAACCTCGCCATCTCGACTTCTCTGTCGGCGCTTCTGATCCCACT 60  
QY 568 GTATGTACCTACGTGCTGACAGGCGCTGGACCTTTCGGCGGGCGCTTCGCAAGCTGTG 627  
DB 61 GTATGTACCTACGTGCTGACAGGCGCTGGACCTTTCGGCGGGCGCTTCGCAAGCTGTG 120  
QY 628 GCTGTAGTGGACTACCTGCTGTGACCTTCTCTGCTTCAACATCGTCTCATCAGCTA 687  
DB 121 GCTGTAGTGGACTACCTGCTGTGACCTTCTCTGCTTCAACATCGTCTCATCAGCTA 180  
QY 688 CGACCGCTTCTGCTGCTGACCGGCGCTCATACCGGCGCGGCGCTGACCGG 747  
DB 181 CGACCGCTTCTGCTGCTGACCGGCGCTCATACCGGCGCGGCGCTGACCGG 240  
QY 748 GCGGGCAGTGGCGAAGATGCTGCTGTGGGTGCTGGCTTCTCTGCTACCGACCGAGC 807

DB 241 GCGGCACTGCGGAAGATGCTGCTGGTGGGTGCTGGCTTCTGCTGTACGGACCGAGC 300  
QY 808 CATCTGAGCTGGAGTACCTGTTCGGGGGAGCTTCATCCCGAGGGCCACTGTGTATGC 867  
DB 301 CATCTGAGCTGGAGTACCTGTTCGGGGGAGCTTCATCCCGAGGGCCACTGTGTATGC 360  
QY 868 CGAGTTCCTTACAACTGGTACTTCTCATCAGCGCTTCCACCTCGGAGTTCCTTACGCC 927  
DB 361 CGAGTTCCTTACAACTGGTACTTCTCATCAGCGCTTCCACCTCGGAGTTCCTTACGCC 420  
QY 928 CTTCTCAGCGCTCACTTCTTTAACTCAGCATCTTACCTGAACATTCAGAGCGCACCG 987  
DB 421 CTTCTCAGCGCTCACTTCTTTAACTCAGCATCTTACCTGAACATTCAGAGCGCACCG 480  
QY 988 CTTCTCAGCGCTCACTTCTTTAACTCAGCATCTTACCTGAACATTCAGAGCGCACCG 1047  
DB 481 CTTCTCAGCGCTCACTTCTTTAACTCAGCATCTTACCTGAACATTCAGAGCGCACCG 540  
QY 1048 CTCACCACTCCAGCGCTGCTGGGGTGTGGCGAGAGGGGCGACGGGAGGCGCAT 1107  
DB 541 CTCACCACTCCAGCGCTGCTGGGGTGTGGCGAGAGGGGCGACGGGAGGCGCAT 600  
QY 1108 GCCGCTGCACAGGTATGGGGTGGGTGAGCGCGCTAGCGCTGAGCGCGGGGAGGCGCAC 1167  
DB 601 GCCGCTGCACAGGTATGGGGTGGGTGAGCGCGCTAGCGCTGAGCGCGGGGAGGCGCAC 660  
QY 1168 CTTCTCAGCGCTCACTTCTTTAACTCAGCATCTTACCTGAACATTCAGAGCGCACCG 1227  
DB 661 CTTCTCAGCGCTCACTTCTTTAACTCAGCATCTTACCTGAACATTCAGAGCGCACCG 720  
QY 1228 CTCGAGGGGCACTGAGAGCGCGCTCACTCAAGAGGGGCTCCAAAGCGCTGGCGCTCTC 1287  
DB 721 CTCGAGGGGCACTGAGAGCGCGCTCACTCAAGAGGGGCTCCAAAGCGCTGGCGCTCTC 780  
QY 1288 GGCCTCGCTGGAGAGCGCATGAAGATGCTGCTCCAGAGCTTCAACCGAGCGTTCGGCT 1347  
DB 781 GGCCTCGCTGGAGAGCGCATGAAGATGCTGCTCCAGAGCTTCAACCGAGCGTTCGGCT 840  
QY 1348 GTCTCGGACAGGAAGTGGCGCAAGTCTGCTGGCGCTCATCTGAGCATCTTTGGGCTCTG 1407  
DB 841 GTCTCGGACAGGAAGTGGCGCAAGTCTGCTGGCGCTCATCTGAGCATCTTTGGGCTCTG 900  
QY 1408 CTGGGCGCGCATACAGCTGCTGATGATCATCGGCGCGCTGCGCATGCGCATGCGTCC 1467  
DB 901 CTGGGCGCGCATACAGCTGCTGATGATCATCGGCGCGCTGCGCATGCGCATGCGTCC 960  
QY 1468 TGACTACTGTGACGAAACCTCTCTTCTGGCTCTCTGTTGGGCGCAACTCGGCTGTCAACCCCTGT 1527  
DB 961 TGACTACTGTGACGAAACCTCTCTTCTGGCTCTCTGTTGGGCGCAACTCGGCTGTCAACCCCTGT 1020  
QY 1528 CCTTACCTCTGTGCGCAACAGCTTCCGGCGCGCTTCAACAGCTGCTTGGCGCGCA 1587  
DB 1021 CCTTACCTCTGTGCGCAACAGCTTCCGGCGCGCTTCAACAGCTGCTTGGCGCGCA 1080  
QY 1588 GAAGCTCAAAATCCAGCGCGCATGCTGAGCACTGCTGGAAGTGAAGTGGCGCGCA 1647  
DB 1081 GAAGCTCAAAATCCAGCGCGCATGCTGAGCACTGCTGGAAGTGAAGTGGCGCGCA 1140  
QY 1648 GAGCTCTCCTCAGCGCACCGCTCTCTCAGCGCGCTCTCTGAGCATCTTGGCGCTTGTGCG 1707  
DB 1141 GAGCTCTCCTCAGCGCACCGCTCTCTCAGCGCGCTCTCTGAGCATCTTGGCGCTTGTGCG 1200  
QY 1708 CCTTACCGCGCTGCTTCCCGAGCGGCTGAGCGCGCTGCTGTTGGCGCTTCTTAAATG 1767  
DB 1201 CCTTACCGCGCTGCTTCCCGAGCGGCTGAGCGCGCTGCTGTTGGCGCTTCTTAAATG 1260  
QY 1768 CCAGCGAGCGCACCGCTGCGCATGAGCGCGCTTCTGCGGTGGCGAGAGGGCGCTTCACTG 1827  
DB 1261 CCAGCGAGCGCACCGCTGCGCATGAGCGCGCTTCTGCGGTGGCGAGAGGGCGCTTCACTG 1320  
QY 1828 GCTGACTGTGAGGCTGGGTGGCGCGCTTGGCGCGCTTCTGCGGTGGCGAGAGGG 1887



Db	1321	GCTGGACTGGAGGCTGGGTGGCGGCGCTGCCCCCACAATTCTGGCTCCACC-GGGAGGG	1379
Qy	1888	ACAGTCTGGAGGTCCCAGACATGCTGCCACACCCCTGCTGTGTCGCCACCCCTTCGCGAGTTA	1947
Db	1380	ACAGTCTGGAGGTCCCAGACATGCTGCCACACCCCTGCTGTGTCGCCACCCCTTCGCGAGTTA	1439
Qy	1948	CTGGTTGGTGTTCCTTCCAAAGCAAGCACTGGGTGTGCTCCAGGCTTCCTGCGCTAGCA	2007
Db	1440	CTGGTTGGTGTTCCTTCCAAAGCAAGCACTGGGTGTGCTCCAGGCTTCCTGCGCTAGCA	1499
Qy	2008	GTTCGCTCTGCAGCTGCACACCTGCACACCCCTGCACACACCTGCACACCGTCCCTC	2067
Db	1500	GTTCGCTCTGCAGCTGCACACCTGCACACCCCTGCACACACCTGCACACCGTCCCTC	1559
Qy	2068	TCCCGGACAAGCCAGGACACTGCTCTTGTGCTCTTCTGTCTCTTGCATGAAGCCTCAGG	2127
Db	1560	TCCCGGACAAGCCAGGACACTGCTCTTGTGCTCTTCTGTCTCTTGCATGAAGCCTCAGG	1619
Qy	2128	CTGGCCCTTTACCCCTCTTCCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGCC	2187
Db	1620	CTGGCCCTTTACCCCTCTTCCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGCC	1679
Qy	2188	CTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATTTCTGGGTGTTTTCAGAAAGATGAAGA	2247
Db	1680	CTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATTTCTGGGTGTTTTCAGAAAGATGAAGA	1739
Qy	2248	AGAAACATGTCTGTGAACCTTGATGTTCTGTGGATGTTTAAATCAAGAGAGACAAATATGC	2307
Db	1740	AGAAACATGTCTGTGAACCTTGATGTTCTGTGGATGTTTAAATCAAGAGAGACAAATATGC	1799
Qy	2308	TGAGGAGCTCAGGGCTGGATTGGCAGGTGTGGGCTCCACGCCCTCTCTCCCTCGCTTAAG	2367
Db	1800	TGAGGAGCTCAGGGCTGGATTGGCAGGTGTGGGCTCCACGCCCTCTCTCCCTCGCTTAAG	1859
Qy	2368	GCTTCCGGCTGAGCTGTGCCAGCTGTCTTCTGCCACCCCGCTCTGGGCTCACACAGCC	2427
Db	1960	GCTTCCGGCTGAGCTGTGCCAGCTGTCTTCTGCCACCCCGCTCTGGGCTCACACAGCC	1919
Qy	2428	CTGTGTGCCAAGCCTGCGCCGCCACTCTGTTTGCTCACCCAGGACCTCTGGGGTGTGTT	2487
Db	1920	CTGTGTGCCAAGCCTGCGCCGCCACTCTGTTTGCTCACCCAGGACCTCTGGGGTGTGTT	1979
Qy	2488	GGGAGGAGGGGGCGCGCTGGGCCGAGGGTCCCAAGCGGTGCAGGGCGGTCCAGAGGA	2547
Db	1980	GGGAGGAGGGGGCGCGCTGGGCCGAGGGTCCCAAGCGGTGCAGGGCGGTCCAGAGGA	2039
Qy	2548	GGTGCCCGGGCAGGGCGCGCTTGCCATGTCTGTGTGACCCCGTGCACCGCTCTGCATG	2607
Db	2040	GGTGCCCGGGCAGGGCGCGCTTGCCATGTCTGTGTGACCCCGTGCACCGCTCTGCATG	2099
Qy	2608	CTCCTCTGCTGTCGCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT	2667
Db	2100	CTCCTCTGCTGTCGCCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT	2159
Qy	2668	TTTTTA 2673	
Db	2160	TTTTTA 2165	
RESULT 15			
ID	AAK94219	standard; cDNA; 1902 BP.	
XX	AAK94219;		
AC	AAK94219;		
XX	06-NOV-2001 (first entry)		
DT	Human full-length cDNA, SEQ ID NO: 2796.		
XX	Human; full length cDNA; cDNA synthesis; oligo-capping; ss.		
XX	Homo sapiens.		

Qy	1010	GAGCAGCCGGCCCCGAGAGCCCCCTCCCGAGGCCCGAGCCCTCA	CCACCCCCCACCGCCTGGC	1069				
Db	481	GAGCAGCCGGCCCCGAGAGCCCCCTCCCGAGGCCCGAGCCCTCA	CCACCCCCCACCGCCTGGC	540				
Qy	1070	TGCTGGGGCTGCTGGCAGAGGGGCGACGGGGAGGCCATGCGCTGC	ACACGGTATGGGTC	1129				
Db	541	TGCTGGGGCTGCTGGCAGAGGGGCGACGGGGAGGCCATGCGCTGC	-----	586				
Qy	1130	GGTGAGCGCGCGTAGGCGCTGAGGCCGGGAGGCCACCCCTCGGGGTG	CGGTGCGGGC	1189				
Db	587	-----	-----	586				
Qy	1190	GGCTCCGTGGCTTCACCCA	CCTCAGCTTCGGGAGCTTCTCGAGGGGCACTGAGAGGCGC	1249				
Db	587	-----	-----	586				
Qy	1250	CGCTCACTCAAGAGGGGCTCCAGCCGTGCGCGTCTCGGCCCTCGCTG	GAGAGAGCGCATG	1309				
Db	587	-----	-----	586				
Qy	1310	AAGATGGTGTCCAGAGGCTTCA	CCAGCGCTTTTCGGGTCTTCGGGACAGAAAGTGCC	1369				
Db	587	-----	-----ACAGGAAGTGCC	600				
Qy	1370	AAGTCGTGGCGTCATCGTAGAGCATTTTGGGCTTGCTGGGCCCCATACA	CGCTGCTG	1429				
Db	601	AAGTCGTGGCGCTCATCGTAGAGCATTTTGGGCTTGCTGGGCCCCATACA	CGCTGCTG	660				
Qy	1430	ATGATCATCCGGGGCCGCTGCCATGGGCCACTGGTGCCCTGAC	TACTGTTAGTACGAAACCTCC	1489				
Db	661	ATGATCATCCGGGGCCGCTGCCATGGGCCACTGGTGCCCTGAC	TACTGTTAGTACGAAACCTCC	720				
Qy	1490	TTCTGGCTCCTGTGGGCAACTCGGCTGTCA	ACCCTGTCTACTACCTCTGTGCCCACAC	1549				
Db	721	TTCTGGCTCCTGTGGGCAACTCGGCTGTCA	ACCCTGTCTACTACCTCTGTGCCCACAC	780				
Qy	1550	AGCTTCGCGCGGGCTTCA	CCAAGCTGCTGTGCCCCCAGAGTCAAAATCGAGCCCCAC	1609				
Db	781	AGCTTCGCGCGGGCTTCA	CCAAGCTGCTGTGCCCCCAGAGTCAAAATCGAGCCCCAC	840				
Qy	1610	AGCTCCCTGGAGCACTGCTGGAAGTAGTGAGTGCGGCCAC	CAGAGCCCTCCCTCAGGCCACCGCCTC	1669				
Db	841	AGCTCCCTGGAGCACTGCTGGAAGTAGTGAGTGCGGCCAC	CAGAGCCCTCCCTCAGGCCACCGCCTC	900				
Qy	1670	TCTCAGGCCAGGTCCTCGGCACTCTGGGCACTCTGGCCCTGTG	TGCCCTACCCGGCTCGTTCGCCCA	1729				
Db	901	TCTCAGGCCAGGTCCTCGGCACTCTGGGCACTCTGGCCCTGTG	TGCCCTACCCGGCTCGTTCGCCCA	960				
Qy	1730	GGGGTAGCCCCCGCTGTCTGTGGCCCTCTCTTAATGCCAC	GGCAGCCACCTGCGCATG	1789				
Db	961	GGGGTAGCCCCCGCTGTCTGTGGCCCTCTCTTAATGCCAC	GGCAGCCACCTGCGCATG	1020				
Qy	1790	GAGCGGCTTCTCTGGGTGGCCAGAGGGCCCTC	CACCTGGCTGGAAGTGGGGTGGC	1849				
Db	1021	GAGCGGCTTCTCTGGGTGGCCAGAGGGCCCTC	CACCTGGCTGGAAGTGGGGTGGC	1080				
Qy	1850	CGGCCCTGCCCCCA	CAATTCGGCTTCAACGGGGAGGGA	CAGTCTGGAGTGTCCAGACAT	1909			
Db	1081	CGGCCCTGCCCCCA	CAATTCGGCTTCCACC--GGGAGGGACAGTCTGAGGTTCCAGACAT	1139				
Qy	1910	GCTGCCACCCCTGCTGGTGCCACCCCTTCGCAAGTTACTGTTGGT	TGTTCTTCCCAAG	1969				
Db	1140	GCTGCCACCCCTGCTGGTGCCACCCCTTCGCAAGTTACTGTTGGT	TGTTCTTCCCAAG	1199				
Qy	1970	CAAGCAGCTGGGTGTCTCCAGGCTTCTG	CGCCCTAGCAGTTTGCTCTGCA	CGTGCAC	2029			
Db	1200	CAAGCAGCTGGGTGTCTCCAGGCTTCTG	CGCCCTAGCAGTTTGCTCTGCA	CGTGCAC	1259			
Qy	2030	ACCTGCA	CCCCCTGCA	CACACTGCA	CA	CGTCCCTCTCCCGGA	CAAGCCAGGAC	2089
Db	1260	ACCTGCA	CCCCCTGCA	CACACTGCA	CA	CGTCCCTCTCCCGGA	CAAGCCAGGAC	1319

Qy	2090	TGCCTTTGCTGCGCTTCTGTGCTCTTGTGCATTAAGCCTCAGGCCTTGCCCTTTTACCCCTCTTC	2149
Db	1320	TGCCTTTGCTGCGCTTCTGTGCTCTTGTGCATTAAGCCTCAGGCCTTGCCCTTTTACCCCTCTTC	1379
Qy	2150	CCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGCCCTPAGGAACCTCGAAGCTGTTC	2209
Db	1380	CCACCAAGCTCTCTCTGCCCCCAAAAGTGTCAAGGGGCCCTPAGGAACCTCGAAGCTGTTC	1439
Qy	2210	CTGCTTTTCCATTCCTGGGTGTGTTTTCAGAAAGATGAAGAAGAAACATGCTGTGAACCTTG	2269
Db	1440	CTGCTTTTCCATTCCTGGGTGTGTTTTCAGAAAGATGAAGAAGAAACATGCTGTGAACCTTG	1499
Qy	2270	ATGTTCTGTGGATGTTTAAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGCTGGAATTG	2329
Db	1500	ATGTTCTGTGGATGTTTAAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGCTGGAATTG	1559
Qy	2330	GCAGGTGTGGCTCCCAACGCCCTCTCCCTCCGCTAAGGCTTCCGGCTGAGCTGTGCCAG	2389
Db	1560	GCAGGTGTGGCTCCCAACGCCCTCTCCCTCCGCTAAGGCTTCCGGCTGAGCTGTGCCAG	1619
Qy	2390	CTGCTTCTGCGCCACCCCGCCTCTGGGCTCACACAGCCCTGTGTGGCCAAAGCCTGCCCGG	2449
Db	1620	CTGCTTCTGCGCCACCCCGCCTCTGGGCTCACACAGCCCTGTGTGGCCAAAGCCTGCCCGG	1679
Qy	2450	CCACTCTGTTTGTCTACCCAGGACCTCTGGGGTGTGTGGAGAGAGGGGCCCGGCTGGG	2509
Db	1680	CCACTCTGTTTGTCTACCCAGGACCTCTGGGGTGTGTGGAGAGAGGGGCCCGGCTGGG	1739
Qy	2510	CCGAGAGGTCCCAAGGGTGCAGGGGGGCTCCAGAGGAGTGTGCCGGGCAAGGGCCGCTT	2569
Db	1740	CCGAGAGGTCCCAAGGGTGCAGGGGGGCTCCAGAGGAGTGTGCCGGGCAAGGGCCGCTT	1799
Qy	2570	CGCCATGTGTGTGCACCCCGTGCACCGCTCTGCATGTCTCTGCTGTGCCCGCTGC	2629
Db	1800	CGCCATGTGTGTGCACCCCGTGCACCGCTCTGCATGTCTCTGCTGTGCCCGCTGC	1859
Qy	2630	GCTGCCCTGCAACCGGTGAGGTCACAATAAGTGTATTTTTT	2672
Db	1860	GCTGCCCTGCAACCGGTGAGGTCACAATAAGTGTATTTTTT	1902

Search completed: June 2, 2005, 06:01:44  
Job time : 1454.49 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 05:10:00 ; Search time 8897.2 Seconds  
(without alignments)  
11546.944 Million cell updates/sec

Title: US-10-727-021-5  
Perfect score: 2699  
Sequence: 1 ccacgcgtccgcgctgca.....aaaaaaaaaaaaaaaaaaaaa 2699

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_ges1:  
9: gb\_ges2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	767.6	28.4	813	5 BX089742	BX089742
2	743.6	27.6	946	5 BQ068856	BQ068856 AGENCOURT
3	706.2	26.2	1103	4 BM548665	BM548665 AGENCOURT
4	680.8	25.2	732	7 CF147822	CF147822 AGENCOURT
5	549.6	20.4	890	4 B1731453	B1731453 603354331
6	543	20.1	672	6 CB556920	CB556920 AMGNNUC:U
7	522	19.3	533	6 CB154982	CB154982 K-EST0213
8	516	19.1	716	7 CN423054	CN423054 170004245
9	476.6	17.7	910	2 BE783826	BE783826 601471053
10	455	16.9	466	7 CN335777	CN335777 170004245
11	429.6	15.9	842	7 C0403631	C0403631 AGENCOURT
12	390.8	14.5	547	6 CB611519	CB611519 AMGNNUC:N
13	389.4	14.4	653	6 BY727560	BY727560 BY727560
14	386	14.3	409	2 BF531112	BF531112 602072279
15	371.2	13.8	499	2 BF567596	BF567596 UI-R-B00-
16	369.6	13.7	519	2 AW669811	AW669811 113386 MA
17	358.8	13.3	412	7 H30846	H30846 yo78d12.r1
18	352	13.0	434	6 CB758850	CB758850 AMGNNUC:S
19	340.8	12.6	1046	5 BQ950659	BQ950659 AGENCOURT
20	336.6	12.5	401	7 R87217	R87217 yo45e10.r1
21	278.8	10.3	775	9 CC580463	CC580463 CH240_375
22	264.2	9.8	853	6 CD326085	CD326085 AGENCOURT
23	252.8	9.4	782	7 CO872448	CO872448 BovGen_00
24	249.4	9.2	538	2 AW654493	AW654493 103977 MA

25	240.6	8.9	490	6 CB725716	CB725716 AMGNNUC:U
26	224.2	8.3	643	1 AL848045	AL848045 AL848045
27	214.4	7.9	258	2 AW654609	AW654609 104607 MA
28	212	7.9	484	1 AA859887	AA859887 UI-R-E0-C
29	205.6	7.6	646	6 CB437482	CB437482 684956 MA
30	202.8	7.5	832	7 CK769909	CK769909 958021 MA
31	197.8	7.3	975	9 CNS039RV	AL234232 Tetradon
32	190.8	7.1	600	2 BE647364	BE647364 UI-M-BH1-
33	189.8	7.0	236	2 BE063702	BE063702 QV3-BT029
34	185.8	6.9	240	7 R87218	R87218 yo45e10.r1
35	185.2	6.9	527	2 AW049250	AW049250 UI-M-BH1-
36	184	6.8	347	6 CB705071	CB705071 AMGNNUC:N
37	183.6	6.8	621	1 AA943666	AA943666 EST199165
38	181	6.7	770	7 CO875612	CO875612 BovGen_03
39	180.8	6.7	281	2 BB592940	BB592940 BB592940
40	179.4	6.6	260	7 H28163	H28163 yo78d12.r1
41	179.2	6.6	733	7 CO875634	CO875634 BovGen_03
42	179.2	6.6	734	7 CO872468	CO872468 BovGen_00
43	176	6.5	744	9 CR021310	CR021310 Forward s
44	174	6.4	1048	4 BM805220	BM805220 AGENCOURT
45	173.6	6.4	1440	9 AY404934	AY404934 Homo sapi

## ALIGNMENTS

RESULT 1  
BX089742  
LOCUS BX089742 813 bp mRNA linear EST 23-JAN-2003  
DEFINITION BX089742 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone  
IMAGP998G19334 ; IMAGE:180906, mRNA sequence.  
ACCESSION BX089742  
VERSION BX089742.1 GI:27821886  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 813)  
AUTHORS Ebert L., Heil, O., Hennig S., Neubert, P., Partsch, E., Peters, M.,  
Radelof, U., Schneider, D. and Korn, B.  
TITLE Human Unigeneset - RZPD3  
JOURNAL Unpublished (2003)  
COMMENT Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany  
RZPD; IMAGP998G19334.  
Human Unigeneset - RZPD3 (RZPDLIB No.972)  
http://www.rzpd.de/CloneCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs  
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH  
Heubnerweg 6, D-14059 Berlin, Germany  
Tel: +49 30 32639 101  
Fax: +49 30 32639 111  
www.rzpd.de

This clone is available royalty-free from RZPD;  
contact RZPD (clone@rzpd.de) for further information. Seq primer:  
M13r, Primer sequence: TTTCACACAGAACACATGAC.

## FEATURES

Location/Qualifiers  
1..813  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGP998G19334 ; IMAGE:180906"  
/sex="Male"  
/dev\_stages="55-year old"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares adult brain N2b4HB55Y"  
/note="Organ: brain; Vector: p773D (Pharmacia) with a  
modified polylinker; Site1: Not 1; Site2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTGGAGCGCGCTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT73 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M. Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla."

ORIGIN	Query Match	28.4%;	Score 767.6;	DB 5;	Length 813;
	Best Local Similarity	98.5%;	Pred. No. 3.3e-143;		
	Matches 803;	Conservative 0;	Mismatches 9;	Indels 3;	Gaps 3;
Qy	1531	CTACCCCTCTGTGCCACACACAGCTTCCCGCGGGCCTTCACCAAG-CTGCTCTGCCCCCCAGA	1589		
Db	1	CTACCCCTCTGTGCCACACACAGCTTCCCGCGGGCCTTCACCAAGTCTGCTCTGCCCCCCAGA	60		
Qy	1590	AGCTCAAAATCCACGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAGTGGCCCCACACAGA	1649		
Db	61	AGCTCAAAATCCACGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAGTGGCCCCACACAGA	120		
Qy	1650	GCCTCCCTCAGCCACAGCCTCTCTCAGGCCCAAGTTCCTCTGGGCATCTGGCCCTGCTGCCCC	1709		
Db	121	GCCTCCCTCAGCCACAGCCTCTCTCAGGCCCAAGTTCCTCTGGGCATCTGGCCCTGCTGCCCC	180		
Qy	1710	CTACCCGGCTCGTTCCTCCCAAGGGGTGAGCCCGCCGCTGCTGTGGCCCTCTCTTAATGCC	1769		
Db	181	CTACCCGGCTCGTTCCTCCCAAGGGGTGAGCCCGCCGCTGCTGTGGCCCTCTCTTAATGCC	240		
Qy	1770	ACGCAAGCCACCTGCCATGGAGGCGCCTTCTCTGGTGTGGCCAGAGGGCCCCCTCACTGGC	1829		
Db	241	ACGCAAGCCACCTGCCATGGAGGCGCCTTCTCTGGTGTGGCCAGAGGGCCCCCTCACTGGC	300		
Qy	1830	TGGACTGGAGGCTGGGTGGCGGCCCTGCCCCCAACATTCGTGCTCAACCGGGAGGGAC	1889		
Db	301	TGGACTGGAGGCTGGGTGGCGGCCCTGCCCCCAACATTCGTGCTCAACCGGGAGGGAC	359		
Qy	1890	AGTCTGGAGGTCCACAGCATGCTGCCACACCCCTGCTGTGTGCCACACCTTCGCAAGTTACT	1949		
Db	360	AGTCTGGAGGTCCACAGCATGCTGCCACACCCCTGCTGTGTGCCACACCTTCGCAAGTTACT	419		
Qy	1950	GTTTGTGTGTTCTTCCCAAAGCAAGCACTGGGTGTGTCTCAGGCTTCCTGCCCTAGCAGT	2009		
Db	420	GTTTGTGTGTTCTTCCCAAAGCAAGCACTGGGTGTGTCTCAGGCTTCCTGCCCTAGCAGT	479		
Qy	2010	TTGCGCTCTGCACGTGCACACACTGACACCCCTGTCACACACCTGACACCGTCCCTCTC	2069		
Db	480	TTGCGCTCTGCACGTGCACACACTGACACCCCTGTCACACACCTGACACCGTCCCTCTC	539		
Qy	2070	CCGGCAAGCCCAAGCACTGCTTTGCTGCCCTTCTGTCTTTGCAATAAGCCTCAGGCC	2129		
Db	540	CCGGCAAGCCCAAGCACTGCTTTGCTGCCCTTCTGTCTTTGCAATAAGCCTCAGGCC	599		
Qy	2130	TGGCCCTTTCACCCCTCTCCCAACCACTCTCTGCCCCCAAGTGTCAAGGGGCCCT	2189		
Db	600	TGGCCCTTTCACCCCTCTCCCAACCACTCTCTGCCCCCAAGTGTCAAGGGGCCCT	659		
Qy	2190	AGGAACCTCGAAGCTGTCTCTGCTTTTCCATCTCTGGGTGTGTTTTCAGAAAGATGAAGAAG	2249		
Db	660	AGGAACCTCGAAGCTGTCTCTGCTTTTCCATCTCTGGGTGTGTTTTCAGAAAGATGAAGAAG	719		
Qy	2250	AAAAATGCTGTGAACCTTGATGTTCTGTTGGATGTTTAAATCAAGAGAGACAAAATTTGCTG	2309		
Db	720	AAAAATGCTGTGAACCTTGATGTTCTGTTGGATGTTTAAATCAAGAGAGACAAAATTTGCTG	779		
Qy	2310	AGGAGCTCAGGGCTGGGATTGGCAGGTGTGGGCTCC	2344		

Db	780	AGGAGTCA-GGCTGGATTGNCAGNGGGCTTC	813
RESULT 2			
BQ068856			
LOCUS			
DEFINITION	BQ068856	946 bp mRNA linear	EST 02-APR-2002
		AGENCOURT 6740127 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802702	
		5', mRNA sequence.	
ACCESSION	BQ068856		
VERSION	BQ068856.1	GI:19897902	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1. (Bases 1 to 946)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LICM2037 row: i column: 07		
	High quality sequence stop: 678.		
FEATURES	Location/Qualifiers		
source	1..946		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:5802702"		
	/tissue_type="neuroblastoma, cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC_47"		
	/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	27.6%;	Score 743.6;	DB 5; Length 946;
Best Local Similarity	93.3%;	Pred. No. 2.2e-158;	
Matches	809;	Conservative 0;	Mismatches 55; Indels 3; Gaps 3;
QY	1303	GCGCATGAGATGGTGTCCAGAGCTTCACCCAGCGCTTCGGCTCTCGGACAGGAA	1362
DB	1	GCGCATGAGATGGTGTCCAGAGCTTCACCCAGCGCTTCGGCTCTCGGACAGGAA	60
QY	1363	AGTGGCCAAAGTCGCTGGCCGCTCATCTGTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAC	1422
DB	61	AGTGGCCAAAGTCGCTGGCCGCTCATCTGTGAGCATCTTTGGGCTCTGCTGGGCCCCATACAC	120
QY	1423	GCTGCTGATGATCATCGGGCGCGCTGCCATGAGCCATCGGTCCTCTGACTGTGGTACGA	1482
DB	121	GCTGCTGATGATCATCGGGCGCGCTGCCATGAGCCATCGGTCCTCTGACTGTGGTACGA	180
QY	1483	AACCTCTTCTGACTCTGTGGGCCAACTCGGCTGTCAACCCGTCTCTACCCCTCTGTG	1542
DB	181	AACCTCTTCTGACTCTGTGGGCCAACTCGGCTGTCAACCCGTCTCTACCCCTCTGTG	240
QY	1543	CCACCACAGCTTCGGCGGGCGCTTCACCAAGCTGTCTTGCCGCCAGAGCTCAAAATCCA	1602









```
RESULT 7
CB154982
LOCUS      CB154982      533 bp      mRNA      linear      EST 29-JAN-2003
DEFINITION K-EST0213081 B2N807043 Homo sapiens cDNA clone B2N807043-31-C05 5',
            mRNA sequence.
ACCESSION  CB154982
VERSION    CB154982.1 GI:28140085
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 533)
AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel.: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.krabb.re.kr
            Plate: 31 row: C column: 05
            High quality sequence stop: 533.
            Location/Qualifiers
FEATURES             source
    1..533
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="B2N807043-31-C05"
        /sex="M"
        /lab_host="Top10F"
        /clone_lib="B2N807043"
        /note="Organ: Brain; Vector: pCNS-D2; Site 1: EcoRI;
            Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
            bacterial alkaline phosphatase (BAP) and then decapped
            with tobacco acid pyrophosphatase (TAP). The decapped
            intact mRNA was ligated with DNA-RNA linker including
            EcoRI site by treatment of T4 RNA ligase and the first
            strand cDNA was synthesized from oligo dt-selected mRNA by
            priming with dt-tailed vector. The dt-tailed vector was
            adjusted to have about 60nt. The cDNA vector was
            circularized with E. coli DNA ligase after digestion of
            EcoRI which site is also included in vector. An RNA strand
            converted to a DNA strand by Okayama-Berg method. The
            obtained cDNA vectors were used for transformation of
            competent cells E. coli Top10F by electroporation method.
            The cDNA libraries constructed by this method are
            full-length enriched cDNA library."
ORIGIN
Query Match      19.3%; Score 522; DB 6; Length 533;
Best Local Similarity 99.8%; Pred. No. 5.4e-94;
Matches 533; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1416 CATACACGCTGCTGATGATCATCCGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACT 1475
DB 1 CATACACGCTGCTGATGATCATCCGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACT 60

QY 1476 GGTAGAAACCTCTTCTGGCTCTGTGGGCAACTCGGCTGTCAACCTGTCTCTTACC 1535
DB 61 GGTAGAAACCTCTTCTGGCTCTGTGGGCAACTCGGCTGTCAACCTGTCTCTTACC 120

QY 1536 CTCCTGTCACACAGCTTCGCGGGGCTTTCACCAAGCTGTCTGCCCCCAGAGCTCA 1595
DB 121 CTCCTGTCACACAGCTTCGCGGGGCTTTCACCAAGCTGTCTGCCCCCAGAGCTCA 180

QY 1596 AAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTAGTGCCGCCACAGAGCTCC 1655
DB |||||||
```

```
181 AAATCCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTAGTGCCGCCACAGAGCTCC 240
QY |||||||
1656 CTCAGCCACGCTCTCTCAGCCCCAGGCTCTCTGGGCACTCTGGCCCTGTGCCCCCTACCC 1715
DB |||||||
241 CTCAGCCACGCTCTCTCAGCCCCAGGCTCTCTGGGCACTCTGGCCCTGTGCCCCCTACCC 300
QY |||||||
1716 GGCTCGTTTCCCCCAGGGGTGAGCCCCCGCGTGTCTGTGGCCCTCTCTTAAATGCCACGGCA 1775
DB |||||||
301 GGCTCGTTTCCCCCAGGGGTGAGCCCCCGCGTGTCTGTGGCCCTCTCTTAAATGCCACGGCA 360
QY |||||||
1776 GCCACCTTGCCATGAGGCGCTTCTTGGGGTGGCCAGAGGGCCCTCTCAGTGGTGGACT 1835
DB |||||||
361 GCCACCTTGCCATGAGGCGCTTCTTGGGGTGGCCAGAGGGCCCTCTCAGTGGTGGACT 420
QY |||||||
1836 GGAGGCTGGGTGGCGGCGCTGCCCCCAGCTTCTGCTCCACCGGGGAGGAGGAGTCTG 1895
DB |||||||
421 GGAGGCTGGGTGGCGGCGCTGCCCCCAGCTTCTGCTCCACCGGGGAGGAGGAGTCTG 479
QY |||||||
1896 GAGGTCCCGAGACATGCTGCCACCCCTGCTGGTGGCCACCCCTTTCGCAGTTACT 1949
DB |||||||
480 GAGGTCCCGAGACATGCTGCCACCCCTGCTGGTGGCCACCCCTTTCGCAGTTACT 533

RESULT 8
CN423054
LOCUS      CN423054      716 bp      mRNA      linear      EST 16-MAY-2004
DEFINITION 17000424504731 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN423054
VERSION    CN423054.1 GI:47410648
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 716)
AUTHORS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
            Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
            Lebkowski,J and Stanton,L.W.
            Transcriptome characterization elucidates signaling networks that
            control human ES cell growth and differentiation
            Nat. Biotechnol. 22 (6), 707-716 (2004)
            Contact: Brandenberger R
            Regenerative Medicine
            Geron Corporation
            230 Constitution Drive, Menlo Park, CA 94025, USA
            Tel: 650 473 8638
            Fax: 650 473 7760
            Email: rbrandenberger@geron.com
            Insert Length: 716 Std Error: 0.00.
            Location/Qualifiers
FEATURES             source
    1..716
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /tissue_type="embryonic stem cells, cell lines H1, H7, and
            H9"
        /clone_lib="GRN_ES"
        /note="Oligo dt primed, full-length enriched cDNA library
            from undifferentiated hES cell lines H1 (p32), H7 (p29),
            and H9 (p26) maintained in feeder-free conditions"
ORIGIN
Query Match      19.1%; Score 516; DB 7; Length 716;
Best Local Similarity 100.0%; Pred. No. 8.8e-93;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 548 GGCGCTTCTGCATCCCACTGTATGTACCTTACCTGTGACAGCGCGCTGACCTTCGGC 607
DB 201 GGCGCTTCTGCATCCCACTGTATGTACCTTACCTGTGACAGCGCGCTGACCTTCGGC 260

QY 608 CGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTCTCTCTGTGACCTCTCTGCTTC 667
DB 261 CGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTCTCTCTGTGACCTCTCTGCTTC 320
```

```
QY 668 AACATCGTCTCATCAGCTACGACCGCTTCCTGTCGGTCAACCGAGCGGTCTCATACCGG 727
|||
Db 321 AACATCGTCTCATCAGCTACGACCGCTTCCTGTCGGTCAACCGAGCGGTCTCATACCGG 380
|||
QY 728 GCCCAGAGGCTGACACCGCGGGGCGAGTCGTCGGTCAACCGAGCGGTCTCATACCGG 787
|||
Db 381 GCCCAGAGGCTGACACCGCGGGGCGAGTCGTCGGTCAACCGAGCGGTCTCATACCGG 440
|||
QY 788 TTCCTGCTGTACGAGCCAGCCATCTCTGAGCTGGGAGTACCTGTCGGGCGGAGCTCCATC 847
|||
Db 441 TTCCTGCTGTACGAGCCAGCCATCTCTGAGCTGGGAGTACCTGTCGGGCGGAGCTCCATC 500
|||
QY 848 CCGCAGGCGCACTGCTATCGAGTTCCTCAACCTGCTATCTCTCAACCGGCTTCC 907
|||
Db 501 CCGCAGGCGCACTGCTATCGAGTTCCTCAACCTGCTATCTCTCAACCGGCTTCC 560
|||
QY 908 ACCCTGGAGTCTTACGCGCTCTCTCAGCGTCACTCTTAACTCAGCATCTACCTG 967
|||
Db 561 ACCCTGGAGTCTTACGCGCTCTCTCAGCGTCACTCTTAACTCAGCATCTACCTG 620
|||
QY 968 AACATCCAGAGCGCACCGCGCTCCGGCTGGATGGGCTCGAGAGCGAGCCGCGCCGAG 1027
|||
Db 621 AACATCCAGAGCGCACCGCGCTCCGGCTGGATGGGCTCGAGAGCGAGCCGCGCCGAG 680
|||
QY 1028 CCCCCTCCGAGGCCAGCCCTCACACCCCCACCG 1063
|||
Db 681 CCCCCTCCGAGGCCAGCCCTCACACCCCCACCG 716
|||

RESULT 9
BE783826 601471053F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874260 5',
LOCUS mRNA sequence. linear EST 20-OCT-2000
DEFINITION BE783826.1 GI:10205024
ACCESSION BE783826
VERSION BE783826
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9631 row: 1 column: 13
High quality sequence stop: 601.
FEATURES
Location/Qualifiers
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3874260"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_67"
/site="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 17.7%; Score 476.6; DB 2; Length 910;

Best Local Similarity 89.1%; Pred. No. 7.1e-85;
Matches 632; Conservative 0; Mismatches 54; Indels 23; Gaps 10;
QY 1177 TGGCGGTGGGGCGGCTCGTGGCTTCAACCACTCCAGCTCCGGCAGCTCTCTCGAGGGG 1236
|||
Db 1 TGGCGGTGGGGCGGCTCGTGGCTTCAACCACTCCAGCTCCGGCAGCTCTCTCGAGGGG 60
|||
QY 1237 CACTCAGAGGGCGCGCTCACTCAAGAGGGGCTCAAGCGGCTCTGGGCTCTGGGCTCGCT 1296
|||
Db 61 CACTCAGAGGGCGCGCTCACTCAAGAGGGGCTCAAGCGGCTCTGGGCTCTGGGCTCGCT 120
|||
QY 1297 GGAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGG 1356
|||
Db 121 GGAGAGCGCATGAGATGGTGTCCAGAGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGG 180
|||
QY 1357 CAGGAAAGTGGGCAAGTGGTGGCGCTCATCTGAGCATCTTTGGGCTCTGGGCTCTGGGCTCTGGG 1416
|||
Db 181 CAGGAAAGTGGGCAAGTGGTGGCGCTCATCTGAGCATCTTTGGGCTCTGGGCTCTGGGCTCTGGG 240
|||
QY 1417 ATACACGCTGTGATGATCATCCGGGCGGCTTCCATGGCCACTGGTCCCTGACTACTG 1476
|||
Db 241 ATACACGCTGTGATGATCATCCGGGCGGCTTCCATGGCCACTGGTCCCTGACTACTG 300
|||
QY 1477 GTACGAAACCTCTCTGGCTCTGGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 1536
|||
Db 301 GTACGAAACCTCTCTGGCTCTGGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 360
|||
QY 1537 TCTGTGCCACACAGCTTCGCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 1596
|||
Db 361 TCTGTGCCACACAGCTTCGCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 415
|||
QY 1597 AATCCAGGCGGCGGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 1656
|||
Db 416 AATCCAGGCGGCGGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 473
|||
QY 1657 TCAGCCAGCGCTCTCTCAGCCAGCTCTCTGGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGG 1716
|||
Db 474 TCAGCCAGCGCTCTCTCAGCCAGCTCTCTGGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGG 528
|||
QY 1717 GTCCTGTCCTCCAGGCGGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 1776
|||
Db 529 GTCCTGTCCTCCAGGCGGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 586
|||
QY 1777 CCACCGCTCCATGGAGGCGGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 1836
|||
Db 587 CC-----GCATGGAGCG-CTTCTGGGTTGGCAAGAGGGGCGCTCACTGGTGGACTG 639
|||
QY 1837 GAGGCTGGGTCGCGCGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 1885
|||
Db 640 ATGCTGGGTCGCGCGCTTCCGCGGCTTCAACCACTCCAGCTCTGGGCTCTGGGCTCTGGGCTCTGGG 686
|||

RESULT 10
CN335777
LOCUS CN335777 466 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000424505478 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN335777
VERSION CN335777.1 GI:47335711
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 466)
Bradenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam,R.,
Lebkowski,J and Stanton,L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
JOURNAL Contact: Bradenberger R
COMMENT Regenerative Medicine
Geron Corporation
```

230 Constitution Drive, Menlo Park, CA 94025, USA  
Tel: 650 473 8658  
Fax: 650 473 7760  
Email: rbrandenberger@eron.com  
Insert Length: 466 Std Error: 0.00.  
Location/Qualifiers  
1. 466

## FEATURES

source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/tissue\_type="embryonic stem cells, cell lines H1, H7, and H9"  
/clone\_lib="GRN ES"  
/note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions"

## ORIGIN

Query Match 16.9%; Score 455; DB 7; Length 466;  
Best Local Similarity 99.8%; Pred. No. 1.4e-80;  
Matches 466; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1593 TCAAAATCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAAGTGGCCACACAGAGCC 1652  
Db 1 TCAAAATCAGCCCCACAGCTCCCTGGAGCACTGCTGGAAGTGAAGTGGCCACACAGAGCC 60  
QY 1653 TCCCTCAGCAGCGCTCTCTAGCCAGGTTCCTGGGCAATCGCCCTGTGCCCCCTTA 1712  
Db 61 TCCCTCAGCAGCGCTCTCTAGCCAGGTTCCTGGGCAATCGCCCTGTGCCCCCTTA 120  
QY 1713 CCCGCTGTTCCTCCAGGGGTAGCCCGCGCTGTCTGTGGCCCTCTCTTAATGCCACG 1772  
Db 121 CCCGCTGTTCCTCCAGGGGTAGCCCGCGCTGTCTGTGGCCCTCTCTTAATGCCACG 180  
QY 1773 GCAGCCACCTGCCATGAGGCGCCTTCCTGGTGGCCAGAGGCGCCCTCACTGGCTGG 1832  
Db 181 GCAGCCACCTGCCATGAGGCGCCTTCCTGGTGGCCAGAGGCGCCCTCACTGGCTGG 240  
QY 1833 ACTGAGGCTGGGTGGCGCGCCCTGCGCCCAATCTTGGCTTCCACCGGGAGGACAGT 1892  
Db 241 ACTGAGGCTGGGTGGCGCGCCCTGCGCCCAATCTTGGCTTCCACCGGGAGGACAGT 299  
QY 1893 CTGAGGTTCCAGACATGTCGCCACCCCTGCTGGTGGCCACCCCTTGCAGTTACTGGT 1952  
Db 300 CTGAGGTTCCAGACATGTCGCCACCCCTGCTGGTGGCCACCCCTTGCAGTTACTGGT 359  
QY 1953 TGGTGTCTTCCAAAGCAAGCACCTGGGTGTGCTCCAGGCTTCTGCGCTAGCAGTTTG 2012  
Db 360 TGGTGTCTTCCAAAGCAAGCACCTGGGTGTGCTCCAGGCTTCTGCGCTAGCAGTTTG 419  
QY 2013 CCTCTGCAGGTGCACACACCTTGCACACCCCTTGCACACACCTTGCACAC 2059  
Db 420 CCTCTGCAGGTGCACACACCTTGCACACCCCTTGCACACACCTTGCACAC 466

## RESULT 11

CO403631  
LOCUS  
DEFINITION CO403631 842 bp mRNA linear EST 01-JUL-2004  
AGENCY 27526928 NIH MGC 254 Rattus norvegicus cDNA clone  
IMAGE:7315203 5', mRNA sequence.  
ACCESSION CO403631  
VERSION CO403631.1 GI:49585547  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 842)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics  
National Cancer Institute / NIH  
Blc9. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical  
College of Wisconsin  
cDNA Library Preparation: Express Genomics  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM15369 row: b column: 01  
High quality sequence stop: 637.  
Location/Qualifiers  
1. 842

## FEATURES

source  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7315203"  
/sex="both"  
/tissue\_type="Brain - Pooled from several tissues from one or more individuals"  
/lab\_host="DH10B Tona"  
/clone\_lib="NIH MGC 254"  
/note="Organ: brain/CNS; Vector: pExpress-1; Site: 1:  
EcorV; Site 2: NotI; RNA obtained from brain tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:  
5'-PGACTAGTCTAGTCCGAGGCGGCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 2.18 kb. This primary library is not normalized (normalized library is NIH MGC 255) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH\_MGC library"

## ORIGIN

Query Match 15.9%; Score 429.6; DB 7; Length 842;  
Best Local Similarity 83.7%; Pred. No. 1.9e-75;  
Matches 538; Conservative 0; Mismatches 90; Indels 15; Gaps 4;  
QY 14 GGCTGCAGGTCGACCGGAGCGGCTCAGGCTCGGCTCTCCCGCTCAGGAGCGG 73  
Db 39 GGGTGACACGACGACCGCGGCGGCTGAGCT-CGGCTTTGCTCTCGCTCAGGAGCGG 97  
QY 74 CGCTGCGGCGCCCACTGGGCTTCGGA-TCCGGCCCGCGGCCCTCGGCACCGCCT----- 126  
Db 98 CGCGCGCGCGCCCACTCGCTCAGATTCGACACGAGCCCTCTGGATCGCCCTCTGG 157  
QY 127 -----GCTCTGGCCCGGCGCGCGCGCGGACCATGCGCTGGGCGCGCCCGAGGAA 180  
Db 158 ACTCTAGCGCGGCTCTTGTCTCCGACCCCGCGGACCATGCTCCGGCGCGCCCC-CGGA 216  
QY 181 ACCGACCGCGGCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
Db 217 ACCGGCTGGGCGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 276  
QY 241 CCCAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
Db 277 CCCAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 336  
QY 301 GGAGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
Db 337 GGAGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 396  
QY 361 GGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCAT 420  
Db 397 GGCTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCTCAT 456  
QY 421 GGCGCTGCTCATCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 480  
Db 457 GGCGCTGCTCATCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 516

Qy	481	CGACTCAGCCTCCGACCCAGAAACAACCTTCTTCTGCTGAACCTCGCCATCTCCGACTT	540
Db	517	GGATTGAGCCTCCGACCCAGAAACAACCTTCTTCTGCTGAACCTCGCCATCTCCGACTT	576
Qy	541	CCTCGTGGGGCCCTTCGATCCACACCTGATGTACCTCTAGTGTGACAGCCGCTGGAC	600
Db	577	CCTCGTGGGTGCTTCGATCATTGATGATACCTCTAGTGTGACAGCCGCTGGAA	636
Qy	601	CTTCGGCGGGCCCTCTGCAAGCTGTGGCTGTAGTGGACTAC	643
Db	637	CTTCNGCGGGCCCTCTGCAAGCTGTGGCTGTAGTGGACTAC	679
RESULT 12			
LOCUS	CB611519	547 bp mRNA linear	EST 07-APR-2003
DEFINITION	AMGNNUC:NRHY3-00179-H8-A W Rat hypothalamus (10735) Rattus norvegicus cDNA clone nrhy3-00179-h8 5', mRNA sequence.		
ACCESSION	CB611519		
VERSION	1	GI:29571407	
KEYWORDS	EST.		
SOURCE	Rattus norvegicus (Norway rat)		
ORGANISM	Rattus norvegicus		
REFERENCE	1 (bases 1 to 547)		
	Angen EST Program.		
	Angen Rat EST Program		
	Unpublished (2003)		
JOURNAL	Contact: Dan Fitzpatrick		
COMMENT	Angen, Inc		
FEATURES	One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA		
	Tel: 805 447-4881		
	Plate: 00179 row: h column: 8.		
	Location/Qualifiers		
ORIGIN	1. 547		
	/organism="Rattus norvegicus"		
	/mol_type="mRNA"		
	/db_xref="taxon:10116"		
	/clone="nrhy3-00179-h8"		
	/tissue_type="hypothalamus"		
Query Match	/clone_lib="W Rat hypothalamus (10735)"		
	/note="vector: pSPORT1; Site_1: SalI; Site_2: NotI; W Rat hypothalamus"		
	14.5%; Score 390.8; DB 6; Length 547;		
	Best Local Similarity 85.6%; Pred. No. 1.1e-67;		
Matches	471; Conservative 0; Mismatches 72; Indels 7; Gaps 3;		
Qy	953	CTCAGCATCTACCTGAACATCCAGAGCGGCACCGCTCCGGCTGGATGGGCTCGAGAG	1012
Db	2	CTCAGCATCTACCTGAACATCCAGAGCGGCACCGCTCCGGCTGGATGGGCGGTGAG	61
Qy	1013	GCAGCGCGCCCGGACCGCTCCCGAGCGCCAGCCCTCACACCCCCA---CGCGCTGGC	1069
Db	62	---GCTGGCCAGAACCCCCACAGATGCCAGCCCTGCGACCTCCAGCTCCCCCAGC	118
Qy	1070	TGCTGGGGCTGCTGGCAGAGGGGCGACGGGAGGCCATGCCGTGCGACAGATATGGGGT	1129
Db	119	TGCTGGGGCTGCTGGCCAAAAGGCGATGGGAGGCCATGCCGTGCGACAGATATGGGGT	178
Qy	1130	GGTGAGCGGCGCTAGGCGCTGAGCGCGGGAGGCGACCTTCGGGGTGGCGTGGGGC	1189
Db	179	GGTGAGCGAGGCGCTGCTGGTGTGAGGCTGGGAGGCGCTCCCTTCGGGGTGGCAGTGGTGA	238
Qy	1190	GGCTCCGTGGCTTCCACCCACTCTCCAGCTCCGGAGAGCTCCCTCGAGGGGCGACTGAGAGCCG	1249
Db	239	GGTCTGCTGCTGCCCACTCCAGCTCTGGCAGCTCTCTCAAGGGGCGACTGAGAGGCCA	298
Qy	1250	CGCTCACTCAAGAGGGGCTCCAAAGCGTGGCGCTCTCGCGCTCGCTGGAGAAAGCGCATG	1309

Db	299	CGCTCACTCAAAAGGGGGCTCCAAAGCCATCAGCATCTTCAGCATCCCTGGAGAAAGCGCATG	358
Qy	1310	AAGATGGTGTCCAGAGCTTACCCAGCGCTTCTCGGCTGTCTCGGACACGAAAGTGGCC	1369
Db	359	AAGATGGTGTCCAGAGCATACCCAGCGCTTCCGGCTGTCTCGGGACAG-AAGTGGCC	417
Qy	1370	AAGTCGTGGCGCTCATCGTAGCATCTTTGGGCTCTGTCTGGGCCCCATACAGCTGCTG	1429
Db	418	AAGTCGTGGCCATCATCGTAGCATCTTTGGGCTCTGTCTGGGCGCGGTACACGCTCCTA	477
Qy	1430	ATGATCATCGGGCCCGCTGCCATGGCCACTCGTCCCTGACTACTGTTACGACGAAACCTCC	1489
Db	478	ATGATCATCGAGCTGCTTGGCCATGGCCGCTGCATCCCGATTACTTGTTACGAGACGTCC	537
Qy	1490	TTCTGGGCTCC	1499
Db	538	TTCTGGCTTC	547
RESULT 13			
LOCUS	BY727560		
DEFINITION	BY727560 RIKEN full-length enriched, adult male cortex Mus musculus cDNA clone B530005H20 5', mRNA sequence.		
ACCESSION	BY727560		
VERSION	1	GI:27140687	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	1 (bases 1 to 653)		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, K., Verardo, R., Wagner, L., Wahlested, C., Wang, Y., Watanabe, Y., Wells, C., Wilting, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itokawa, T., Fukuda, S., Hara, A., Hashizume, W., Inotani, K., Ishii, Y., Arakawa, T., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.		
	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
MEDLINE	22354683		
PUBMED	12466851		
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.jp, URL: http://genome.gsc.riken.jp/		



Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN

```
Query Match      14.3%; Score 386; DB 2; Length 409;
Best Local Similarity 98.5%; Pred. No. 9.6e-67;
Matches 400; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

Qy 2127 GCCTGGCCCTTTACCCCTCTTCCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGC 2186
Db 5 GGCCTGGCCCTTTACCCCTCTTCCACCAACTCTCTCTGCCCCCAAAAGTGTCAAGGGGC 64

Qy 2187 CCTAGGAACCTCGAAGCTGTTCTCTGCTTTTCCATCTGCGGTGTTTTCAGAAAGATGAAG 2246
Db 65 CCTAGGAACCTCGAAGCTGTTCTCTGCTTTTCCATCTGCGGTGTTTTCAGAAAGATGAAG 124

Qy 2247 AAGAAACATGCTCTGAACCTGATGTTCTGCGGATGTTTAAATCAAGAGACAAATTTG 2306
Db 125 AAGAAACATGCTCTGAACCTGATGTTCTGCGGATGTTTAAATCAAGAGACAAATTTG 184

Qy 2307 CTGAGGAGCTCAGGGCTCGAATGGCAGGTGTGGGCTCCACGCCCTCTCTCCCGCTAA 2366
Db 185 CTGAGGAGCTCAGGGCTCGAATGGCAGGTGTGGGCTCCACGCCCTCTCTCCCGCTAA 244

Qy 2367 GCCTTCCGGCTGAGCTGTGCGAGCTGTCTTCCACCCCGCTCTGGGCTCACACCGC 2426
Db 245 GCCTTCCGGCTGAGCTGTGCGAGCTGTCTTCCACCCCGCTCTGGGCTCACACCGC 304

Qy 2427 CTGCTGGCCCAAGCTGCGCCGCCACTGTGTTGCTTACCAGACCTCTGGGGTTGT 2486
Db 305 CTGCTGGCCCAAGCTGCGCCCGG-CACTCTGTTTCTCACCCAGACCTCTGGGGTTGT 363

Qy 2487 TGGGAGGAGGGGGCCCGCTGGGCGCCGAGGGTCCCAAGCGTGCAG 2532
Db 364 TGGGAGGAGGGGGCCCGCTGGGCGCCGAGGGTCCCAAGCGTGCAG 409
```

RESULT 15

```
BF567596
LOCUS      BF567596      499 bp      mRNA      linear      EST 12-DEC-2000
DEFINITION UI-R-B00-agr-c-06-0-UI-r1 UI-R-B00 Rattus norvegicus cDNA clone
            UI-R-B00-agr-c-06-0-UI 5', mRNA sequence.
ACCESSION  BF567596
VERSION    BF567596.1 GI:11677326
KEYWORDS   EST.
SOURCE     Rattus norvegicus (Norway rat)
ORGANISM   Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE  1 (bases 1 to 499)
AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE     Normalization and subtraction: two approaches to facilitate gene
JOURNAL   Genome Res. 6 (9), 791-806 (1996)
MEDLINE   97044477
PUBMED    889548
COMMENT   Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1796445
            Seq primer: M13 Forward
            Location/Qualifiers
            1..499
            /organism="Rattus norvegicus"
            /mol_type="mRNA"
```

FEATURES

source

```
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B00-agr-c-06-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="UI-R-B00"
/notice="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratstat.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"
```

ORIGIN

```
Query Match      13.8%; Score 371.2; DB 2; Length 499;
Best Local Similarity 90.0%; Pred. No. 9e-64;
Matches 397; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 548 GGGCGCTTCTGCATCCCACTGTATGTACCTACGTGTGACAGCGCGGTGGACCTTCGGC 607
Db 59 GGTGCTTCTGCATCCCACTGTATGTACCTATGTGTGACCGCGCGTGGACCTTCGGC 118

Qy 608 CGGGCGCTTCTCAAGCTGTGCTGTAGTGAACCTGTGTGACCTCTCTCTCTCTCTCT 667
Db 119 CGGGCGCTTCTCAAGCTGTGCTGTAGTGAACCTGTGTGACCTCTCTCTCTCTCTCT 178

Qy 668 AACATCGTCTCATCAGCTACGACCGCTTCTCTCGGTCAACCGAGCGGTCTCATACCG 727
Db 179 AACATCGTCTCATCAGCTATGACCGGATTCCTGTGACGTCACTCGAGTGTCTCTCTAC 238

Qy 728 GCCAGAGGGGTGACACCGCGGGCAGTGGGGAAGATGCTGCTGTGTGGGTGCTGGCC 787
Db 239 GCCAGAGGGGGACACGAGACGGGCGCTTCGGAAGATGGCACTGTGTGTGGGTGCTGGCC 298

Qy 788 TTCCTGTGTACGGACACGACCATCTGTAGCTGGGAGTACCTGTTCGGGGGAGCTCCATC 847
Db 299 TTCCTGTGTATGGGCTTGCCATCTGTAGTTGGGAGTACCTGTCTGTGGGAGTTCATC 358

Qy 848 CCCGAGGGCCACTGCTATGCGGAGTTCCTTCTACAACTGGTACTTCTCTCATCAGGCTTCC 907
Db 359 CCCGAGGGCCACTGCTATGCTGAGTTCCTTCTACAACTGGTACTTCTCTCATCAGGCTTCC 418

Qy 908 ACCCTGGAGTTCCTTACCGCCCTTCTCGAGCTCACTCTTCTTAACTCAGCATCTACCTG 967
Db 419 ACCCTCGAGTTCCTTACCGCCCTTCTCTCAGCGTTACCTTCTTCAACCTCAGCATCTACCTG 478

Qy 968 AACATCCAGAGCGCCACCCGC 988
Db 479 AACATCCAGAGCGCCACCCGC 499
```

Search completed: June 2, 2005, 14:34:37  
Job time : 8905.2 secs

**THIS PAGE BLANK (USPTO)**





```
Db 241 TTCTCGTCGGCGCCTTCTGCATCCCACTGTATGTACCCCTACGTGCTGACAGCGCGCTGG 300
QY 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGAGTACTGCTGTGCACTCC 360
Db 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGAGTACTGCTGTGCACTCC 360
QY 361 TCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTCTGCTACCCGAGCGGTC 420
Db 361 TCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTCTGCTACCCGAGCGGTC 420
QY 421 TCATACCGGGCCAGCAGGGTGCACGCGCGGGCAGTGCAGGAAGTGTCTGTGTGG 480
Db 421 TCATACCGGGCCAGCAGGGTGCACGCGCGGGCAGTGCAGGAAGTGTCTGTGTGG 480
QY 481 GTGCTGGCTTCTGCTGTACGACAGCAGCATCTGAGCTGGAGTACTGCTCCGGGGC 540
Db 481 GTGCTGGCTTCTGCTGTACGACAGCAGCATCTGAGCTGGAGTACTGCTCCGGGGC 540
QY 541 AGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTCTACAACCTGGTACTTCTCATC 600
Db 541 AGCTCCATCCCGAGGGCCACTGCTATGCGGAGTTCTTCTACAACCTGGTACTTCTCATC 600
QY 601 ACGGCTTCCACCTGGAGTCTTTACGCCCTTCTCAGCGTCACTTCTTTAACTCAGC 660
Db 601 ACGGCTTCCACCTGGAGTCTTTACGCCCTTCTCAGCGTCACTTCTTTAACTCAGC 660
QY 661 ATCTACTGAACATTCAGAGGCGACCGCTCCGGCTGGATGGGCTCGAGAGGAGCC 720
Db 661 ATCTACTGAACATTCAGAGGCGACCGCTCCGGCTGGATGGGCTCGAGAGGAGCC 720
QY 721 GCGCCGAGCCCTTCCGAGGCGCAGCCCTCACACCCCGCTGGCTGGCTGGGGC 780
Db 721 GCGCCGAGCCCTTCCGAGGCGCAGCCCTCACACCCCGCTGGCTGGCTGGGGC 780
QY 781 TGTGTCAGAGGGGCGACGGGAGGCGCATGCGCTGCACAGGTATGGGTGGGTGAGGGC 840
Db 781 TGTGTCAGAGGGGCGACGGGAGGCGCATGCGCTGCACAGGTATGGGTGGGTGAGGGC 840
QY 841 GCGGTAGGCGCTGAGCGCGGGAGGAGCCCTCGGGGGTGGCGTGGGGCGGCTCCGTC 900
Db 841 GCGGTAGGCGCTGAGCGCGGGAGGAGCCCTCGGGGGTGGCGTGGGGCGGCTCCGTC 900
QY 901 GCTTACCCACCTCCAGCTCCGCGAGCTCCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
Db 901 GCTTACCCACCTCCAGCTCCGCGAGCTCCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
QY 961 AAGAGGGGCTCCAAGCGCTCGCGCTCCTCGGCTCGCTGGAAGCGCATGAAGTGGT 1020
Db 961 AAGAGGGGCTCCAAGCGCTCGCGCTCCTCGGCTCGCTGGAAGCGCATGAAGTGGT 1020
QY 1021 TCCAGAGCTTCAACAGCGCTTGGCTGTCTCGGACAGGAAAGTGGCCAGTTCGTC 1080
Db 1021 TCCAGAGCTTCAACAGCGCTTGGCTGTCTCGGACAGGAAAGTGGCCAGTTCGTC 1080
QY 1081 GCGTCATCGTGAAGATCTTTGGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATC 1140
Db 1081 GCGTCATCGTGAAGATCTTTGGGCTCTGCTGGGCCCCATACACGCTGCTGATGATCATC 1140
QY 1141 CGGGCGCTCGCATGGCCACTCGCTCCCTGACTACTGTTAGCAAACTCTTCTGGGTC 1200
Db 1141 CGGGCGCTCGCATGGCCACTCGCTCCCTGACTACTGTTAGCAAACTCTTCTGGGTC 1200
QY 1201 CTGTGGGCAACTCGGCTGTAAACCTGTCTTACCTCTGTGTGCAACAGTTCGTC 1260
Db 1201 CTGTGGGCAACTCGGCTGTAAACCTGTCTTACCTCTGTGTGCAACAGTTCGTC 1260
QY 1261 CGGGCTTCAACAGTGTCTGCCCCCAGAGAGCTCAAAATCCAGCCCCCAGAGTCCCTG 1320
Db 1261 CGGGCTTCAACAGTGTCTGCCCCCAGAGAGCTCAAAATCCAGCCCCCAGAGTCCCTG 1320
QY 1321 GAGCACTGCTGGAAG 1335
Db 1321 GAGCACTGCTGGAAG 1335
```

---

```
RESULT 2
BD235873
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
BD235873
Isolated DNA encoding human H3 histamine receptor.
BD235873
BD235873.1 GI:33045643
JP 2002526049-A/6.
synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 1335)
Labenberg,T.W., Erlander,M., Huber,A. and Piatei,J.
Isolated DNA encoding human H3 histamine receptor
Patent: JP 2002526049-A 6 20-AUG-2002;
ORTHO MCNEIL PHARMACEUTICAL INC
OS Artificial Sequence
PN JP 2002526049-A/6
PD 20-AUG-2002
PF 07-OCT-1998 JP 2000573370
PI TIMOTHY W LABENBERG, MARK ERLANDER, ARNE HUBER, JIYAYASYURY PI
PIATEI
PC C12N15/09,A61K38/00,A61K45/00,A61P3/04,A61P3/10,A61P9/06, PC
A61P25/16
PC A61P25/18,A61P25/22,A61P25/24,A61P25/28,C07K14/705,C07K16/28,
PC C12N1/15,
PC C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68 PC
,G01N33/15,G01N33/50,
PC C12N15/00,A61K37/02,C12N5/00
CC Description of Artificial Sequence:CDNA
FH Key Location/Qualifiers
FT source 1..1335
FT /organism='Artificial Sequence'.
FEATURES
source
1..1335
/organism='synthetic construct'
/mol_type='genomic DNA'
/db_xref='taxon:32630'
ORIGIN
Query Match 100.0%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; Pred. No. 7,7e-178;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCTGGCGGCGATGCG 60
Db 1 ATGAGAGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCTGGCGGCGATGCG 60
QY 61 GCGGGCGGGGGCGGGCGGGCTTCTCGCGAGCGCTGGAGCGCGGTGCTGGCGCGCTC 120
Db 61 GCGGGCGGGGGCGGGCGGGCTTCTCGCGAGCGCTGGAGCGCGGTGCTGGCGCGCTC 120
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGTGGGCAACGCGCTGATGCTCGCCTTCGTC 180
Db 121 ATGGCGCTGCTCATCGTGGCCACGCTGTGGGCAACGCGCTGATGCTCGCCTTCGTC 180
QY 181 GCCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 240
Db 181 GCCGACTCGAGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 240
QY 241 TTCTCTGTCGGGGCTTCTGATCCCACTGTATGTACCTAGCTAGTGTGACAGGCGCTGG 300
Db 241 TTCTCTGTCGGGGCTTCTGATCCCACTGTATGTACCTAGCTAGTGTGACAGGCGCTGG 300
QY 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGAGTACTGCTGTGCACTCC 360
Db 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGAGTACTGCTGTGCACTCC 360
QY 361 TCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTGTGGTTCACCGAGCGGTC 420
Db 361 TCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTGTGGTTCACCGAGCGGTC 420
```

```
QY 421 TCATACCGGGCCAGCAGGGTGCACCGCGGGGCGAGTGCAGAGATGCTGTGTGG 480
Db 421 TCATACCGGGCCAGCAGGGTGCACCGCGGGGCGAGTGCAGAGATGCTGTGTGG 480
QY 481 GTGCTGGCCCTTCTGTGTACGACAGCAGCATCTTGAGCTGGAGTACCTGTCCGGGGGC 540
Db 481 GTGCTGGCCCTTCTGTGTACGACAGCAGCATCTTGAGCTGGAGTACCTGTCCGGGGGC 540
QY 541 AGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCCTTACAACCTGTGCTTCTCATC 600
Db 541 AGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCCTTACAACCTGTGCTTCTCATC 600
QY 601 AGGGCTTCCACCTGGAGTTCCTTACGGCCCTTCTCAGGCTCACCTTCTTTAACTCAGC 660
Db 601 AGGGCTTCCACCTGGAGTTCCTTACGGCCCTTCTCAGGCTCACCTTCTTTAACTCAGC 660
QY 661 ATCTACCTGAACATCCAGAGGGCCAGCCGCTCCGGCTGCGATGGGCTCGAGAGCAGCC 720
Db 661 ATCTACCTGAACATCCAGAGGGCCAGCCGCTCCGGCTGCGATGGGCTCGAGAGCAGCC 720
QY 721 GGGCCCGAGCCCTTCCGAGGCCAGCCCTTCAACACCCCGCTGGCTGTGGGGC 780
Db 721 GGGCCCGAGCCCTTCCGAGGCCAGCCCTTCAACACCCCGCTGGCTGTGGGGC 780
QY 781 TGCTGGCAGAGGGGCAAGGGAGGCGATGCGCTGCGACAGGTATGGGTGGGTGAGGCG 840
Db 781 TGCTGGCAGAGGGGCAAGGGAGGCGATGCGCTGCGACAGGTATGGGTGGGTGAGGCG 840
QY 841 GCGGTAGGCGGTAGGCGGGGAGGCGACCTCGGGGGTGGGGTGGGGGGGCTCCGTC 900
Db 841 GCGGTAGGCGGTAGGCGGGGAGGCGACCTCGGGGGTGGGGTGGGGGGGCTCCGTC 900
QY 901 GCTTACCCACCTCCAGCTCCGCGAGCTCTCGAGGGGCACTGAGAGGCGCGGCTCACTC 960
Db 901 GCTTACCCACCTCCAGCTCCGCGAGCTCTCGAGGGGCACTGAGAGGCGCGGCTCACTC 960
QY 961 AAGAGGGGCTCAAGCGCTGCGGCTCTCGGCTCGTGGAGAGCGCATGAAGATGGTG 1020
Db 961 AAGAGGGGCTCAAGCGCTGCGGCTCTCGGCTCGTGGAGAGCGCATGAAGATGGTG 1020
QY 1021 TCCAGAGGCTCAAGCGCTGCGGCTCTCGGCTCGTGGAGAGCGCATGAAGATGGTG 1080
Db 1021 TCCAGAGGCTCAAGCGCTGCGGCTCTCGGCTCGTGGAGAGCGCATGAAGATGGTG 1080
QY 1081 GCGGTATCGTGAGCATCTTTGGGCTCTGCTGGGCGCCATACACGCTGTGATGATCATC 1140
Db 1081 GCGGTATCGTGAGCATCTTTGGGCTCTGCTGGGCGCCATACACGCTGTGATGATCATC 1140
QY 1141 CGGGCGGCTGCGATGGGCACTGCGTCTGCTGACTACTGCTGCTGCTGCTGCTGCTGCTG 1200
Db 1141 CGGGCGGCTGCGATGGGCACTGCGTCTGCTGACTACTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1201 CTGTGGGCAACTCGGCTGTCAACCTGCTTACCTTCTTACCTTCTGTCACACAGCTTCGCG 1260
Db 1201 CTGTGGGCAACTCGGCTGTCAACCTGCTTACCTTCTTACCTTCTGTCACACAGCTTCGCG 1260
QY 1261 CGGGCTTCCACCAAGCTGTCTGCGCCCGCAGAGCTCAAAATCCAGCCCGCATAGCTTCCCTG 1320
Db 1261 CGGGCTTCCACCAAGCTGTCTGCGCCCGCAGAGCTCAAAATCCAGCCCGCATAGCTTCCCTG 1320
QY 1321 GAGCACTGCTGGAAG 1335
Db 1321 GAGCACTGCTGGAAG 1335
```

```
RESULT 3
AR217195 LOCUS 1335 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 6 from patent US 6413743.
ACCESSION AR217195
VERSION AR217195.1 GI:23316635
KEYWORDS Unknown.
```

```
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Lovenberg,T.W., Erlander,M., Huvar,A. and Pyati,J.
TITLE DNA encoding a human histamine receptor of the H3 subtype
JOURNAL Patent: US 6413743-A 6 02-JUL-2002;
FEATURES
    Location/Qualifiers
        1..1335
            /organism="unknown"
            /mol_type="genomic DNA"
```

## ORIGIN

```
Query Match 100.0%; Score 1335; DB 6; Length 1335;
Best Local Similarity 100.0%; Pred. No. 7,7e-178;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGACCGCGGTGCTGGCGGCGATGCG 60
Db 1 ATGAGAGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGACCGCGGTGCTGGCGGCGATGCG 60
QY 61 GCGGCGGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGACCGCGGTGCTGGCGGCGATGCG 120
Db 61 GCGGCGGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGACCGCGGTGCTGGCGGCGATGCG 120
QY 121 ATGCGCTGTCTATCGTGGCCACCGGTGCTGGGCAACGCGTGTATGCTCGCCTTCGTG 180
Db 121 ATGCGCTGTCTATCGTGGCCACCGGTGCTGGGCAACGCGTGTATGCTCGCCTTCGTG 180
QY 181 GCGGACTCGAGGCTCCGCGCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
Db 181 GCGGACTCGAGGCTCCGCGCGCGCGCGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 240
QY 241 TTCTCTGTGCGCGCTTCTGATCCACTGTATGTACCTAGCTGTGTGAGTGTGCTGCTGCTGCTG 300
Db 241 TTCTCTGTGCGCGCTTCTGATCCCACTGTATGTACCTAGCTGTGTGAGTGTGCTGCTGCTG 300
QY 301 ACCTTGGCGCGGGGCTCTGCAAGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 301 ACCTTGGCGCGGGGCTCTGCAAGCTGTGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 TCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 420
Db 361 TCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTG 420
QY 421 TCATACCGGGCCAGCAGGGTGCACCGCGGGGCGAGTGCAGAGATGCTGTGTGTGG 480
Db 421 TCATACCGGGCCAGCAGGGTGCACCGCGGGGCGAGTGCAGAGATGCTGTGTGTGG 480
QY 481 GTGCTGGCCTTCTGCTGTACGACCGAGCCATCTCTGAGCTGGAGTACCTGTCCGGGGGC 540
Db 481 GTGCTGGCCTTCTGCTGTACGACCGAGCCATCTCTGAGCTGGAGTACCTGTCCGGGGGC 540
QY 541 AGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCCTTACAACCTGTGCTTCTTCTCATC 600
Db 541 AGCTCCATCCCGAGGGCCACTGCTATGCGAGTTCCTTACAACCTGTGCTTCTTCTCATC 600
QY 601 ACGGCTTCCACCTGGAGTTCCTTACGGCCCTTCTCAGGCTCACCTTCTTTAACTCAGC 660
Db 601 ACGGCTTCCACCTGGAGTTCCTTACGGCCCTTCTCAGGCTCACCTTCTTTAACTCAGC 660
QY 661 ATCTACCTGAACATCCAGAGGGCCAGCCGCTCCGGCTGCGATGGGCTCGAGAGCAGCC 720
Db 661 ATCTACCTGAACATCCAGAGGGCCAGCCGCTCCGGCTGCGATGGGCTCGAGAGCAGCC 720
QY 721 GGGCCCGAGCCCTTCCGAGGGCCAGCCCTTCAACACCCCGCTGGCTGTGGGGC 780
Db 721 GGGCCCGAGCCCTTCCGAGGGCCAGCCCTTCAACACCCCGCTGGCTGTGGGGC 780
QY 781 TGCTGGCAGAGGGGCAAGGGAGGCGATGCGCTGCGACAGGTATGGGTGGGTGAGGCG 840
Db 781 TGCTGGCAGAGGGGCAAGGGAGGCGATGCGCTGCGACAGGTATGGGTGGGTGAGGCG 840
QY 841 GCGGTAGGCGGTAGGCGGGGAGGCGACCTCGGGGGTGGGGTGGGGGGGCTCCGTC 900
```

```
Db      841  GCGTAGGCGCTGAGGCGGGGAGGCGACCTTCGGGGTGGCGGTGGGGCGGCTCCGCTG 900
Qy      901  GTTCAACCACTCCAGCTCCGGCACTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
Db      901  GCTTACCACCTCCAGCTCCGGCACTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
Qy      961  AAGAGGGGCTCAAGCGCTCGGGCTCTCGGCTCTCGCTGGAGAGGCGCATGAAGATGGT 1020
Db      961  AAGAGGGGCTCAAGCGCTCGGGCTCTCGGCTCTCGCTGGAGAGGCGCATGAAGATGGT 1020
Qy      1021  TCCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTCGGCAAGAAAGTGCCAAAGTCGCTG 1080
Db      1021  TCCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTCGGCAAGAAAGTGCCAAAGTCGCTG 1080
Qy      1081  GCCGTATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCCATACACGCTGTGATGATCATC 1140
Db      1081  GCCGTATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCCATACACGCTGTGATGATCATC 1140
Qy      1141  CGGGCGGCTGCCATGGGCACTGGCTCCGCTGCTACTGCTAGCAAACTCTTCTGGGCTC 1200
Db      1141  CGGGCGGCTGCCATGGGCACTGGCTCCGCTGCTACTGCTAGCAAACTCTTCTGGGCTC 1200
Qy      1201  CTGTGGGCAACTCTGGCTGTCAACCTGTCTTACCTCTGTGCCCCCATACAGCTTCCGC 1260
Db      1201  CTGTGGGCAACTCTGGCTGTCAACCTGTCTTACCTCTGTGCCCCCATACAGCTTCCGC 1260
Qy      1261  CGGGCTTCAACCAAGCTGTCTGCCCCCAGAGCTCAAAATCCAGCTCCCTG 1320
Db      1261  CGGGCTTCAACCAAGCTGTCTGCCCCCAGAGCTCAAAATCCAGCTCCCTG 1320
Qy      1321  GAGCACTGCTGAAG 1335
Db      1321  GAGCACTGCTGAAG 1335

RESULT 4
AR135732
LOCUS      AR135732          2699 bp      DNA      linear      PAT 16-JUN-2001
DEFINITION Sequence 5 from patent US 6136559.
ACCESSION AR135732
VERSION   AR135732.1  GI:14476404
KEYWORDS  'Unknown.'
SOURCE    'Unknown.'
ORGANISM  'Unclassified.'
REFERENCE 1 (bases 1 to 2699)
AUTHORS   Lovenberg,T.W., Erlander,M., Huvar,A. and Pyati,J.
TITLE     DNA encoding as human histamine receptor of the H3 subtype
JOURNAL   Patent: US 6136559-A 5 24-OCT-2000;
FEATURES  Location/Qualifiers
           1..2699
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 1335; DB 6; Length 2699;
Best Local Similarity 100.0%; Pred. No. 6,7e-178;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ATGGAGCGCGCGCGCGCGCGCGCTGAAAGCTTCGGGGGCGCTGGCGGGCGATGCG 60
Db      299  ATGGAGCGCGCGCGCGCGCGCGCTGAAAGCTTCGGGGGCGCTGGCGGGCGATGCG 358
Qy      61  GCGGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGGACCGCGGTGTGGCGCGCTC 120
Db      359  GCGGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGGACCGCGGTGTGGCGCGCTC 418
Qy      121  ATGGCGCTGCTATCGTGGCGCAGGTCGTGGGCAACGCGCTGGTATGTCGCTTCG 180
Db      419  ATGGCGCTGCTATCGTGGCGCAGGTCGTGGGCAACGCGCTGGTATGTCGCTTCG 478
Qy      181  GCGGACTCGAGCTTCGGCACCGCAACAACTTCTTCTGCTCAACCTCGCCATCTCCG 240
```

```
Db      479  GCCGACTCGAGCTCCGCAACCAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 538
Qy      241  TTCTCTGTCGGCGCTTCTGCACTCCCACTGTATGTACCTTACGTGCTGACAGGCGCTGG 300
Db      539  TTCTCTGTCGGCGCTTCTGCACTCCCACTGTATGTATACCTTACGTGCTGACAGGCGCTGG 598
Qy      301  ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAGTGGACTACCTGCTGTGCACTTCC 360
Db      599  ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAGTGGACTACCTGCTGTGCACTTCC 658
Qy      361  TCTGCTTTCAACATCGTCTCATCAGCTACGACCGCTTCTGTCGGTCAACCGAGCGGTC 420
Db      659  TCTGCTTTCAACATCGTCTCATCAGCTACGACCGCTTCTGTCGGTCAACCGAGCGGTC 718
Qy      421  TCATACCGGGGCCAGAGGGGTGACACGCGGGGCGAGTGCAGAAAGATGCTGCTGTGTGG 480
Db      719  TCATACCGGGGCCAGAGGGGTGACACGCGGGGCGAGTGCAGAAAGATGCTGCTGTGTGG 778
Qy      481  GTGCTGGCTTCTCTGCTGTACGGACCACTCTGAGCTGGGAGTACCTGTCGGGGGCG 540
Db      779  GTGCTGGCTTCTCTGCTGTACGGACCACTCTGAGCTGGGAGTACCTGTCGGGGGCG 838
Qy      541  AGCTCCATCCCGAGGGCCACTGCTATGCCAGTTCCTTCTACAACTGGTACTTCTCTCATC 600
Db      839  AGCTCCATCCCGAGGGCCACTGCTATGCCAGTTCCTTCTACAACTGGTACTTCTCTCATC 898
Qy      601  ACGGCTTCCACCTCTGGAGTTCTTTACGCCCTTCTCTCAGCTCACTTCTTTAACTCAGC 660
Db      899  ACGGCTTCCACCTCTGGAGTTCTTTACGCCCTTCTCTCAGCTCACTTCTTTAACTCAGC 958
Qy      661  ATCTACTGTGAATCCAGAGGGGCAACCGCTCCGGCTGGATGGGGCTCGAGAGCAGCC 720
Db      959  ATCTACTGTGAATCCAGAGGGGCAACCGCTCCGGCTGGATGGGGCTCGAGAGCAGCC 1018
Qy      721  GGGCCGAGCGCCCTCCCGAGGCCAGCCCTCACACCCCGCCCTGGCTGGCTGGGGC 780
Db      1019  GGGCCGAGCGCCCTCCCGAGGCCAGCCCTCACACCCCGCCCTGGCTGGCTGGGGC 1078
Qy      781  TGCTGGCAGAGAGGGGCAACGGGGAGGCCATGCGCTGCAAGGTATGGGGTGGGTGAGGCG 840
Db      1079  TGCTGGCAGAGAGGGGCAACGGGGAGGCCATGCGCTGCAAGGTATGGGGTGGGTGAGGCG 1138
Qy      841  GCGGTAGGCGCTGAGGCGGGGAGCGACCTTCGGGGGTGGGGGTGGGGGGCGCTCCGCTG 900
Db      1139  GCGGTAGGCGCTGAGGCGGGGAGCGACCTTCGGGGGTGGGGGTGGGGGGCGCTCCGCTG 1198
Qy      901  GCTTCAACCACTCCAGCTCCGGCACTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
Db      1199  GCTTCAACCACTCCAGCTCCGGCACTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 1258
Qy      961  AAGAGGGGCTCAAGCGCTCGGCTCTCGGCTCGCTGGAGAGCGCATGAAGATGGT 1020
Db      1259  AAGAGGGGCTCAAGCGCTCGGCTCTCGGCTCGCTGGAGAGCGCATGAAGATGGT 1318
Qy      1021  TCCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTCGGCAAGAAAGTGCCAAAGTCGCTG 1080
Db      1319  TCCAGAGCTTCAACCAAGCGCTTTCGGCTGTCTCGGCAAGAAAGTGCCAAAGTCGCTG 1378
Qy      1081  GCGGTATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCCATACACGCTGTGATGATCATC 1140
Db      1379  GCGGTATCGTGAGCATCTTTGGGCTCTGCTGGGCCCCCATACACGCTGTGATGATCATC 1438
Qy      1141  CGGGCGGCTGCCATGGGCACTGGCTGCTGACTACTGTAAGTGTGTAAGTGTGCTTC 1200
Db      1439  CGGGCGGCTGCCATGGGCACTGGCTGCTGACTACTGTAAGTGTGTAAGTGTGCTTC 1498
Qy      1201  CTGTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTGTGCGCAACAGCTTCGCG 1260
Db      1499  CTGTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTGTGCGCAACAGCTTCGCG 1558
Qy      1261  CGGGCTTCAACCAAGCTCTCTGCCCCCAGAGCTCAAAATCCAGCTCCCTG 1320
```

Db 1559 CGGGCTTACCAAGTGTCTGCCCCAGAAAGCTCAAAATCCAGCCCCACAGTCCCTG 1618  
QY 1321 GAGCACTGCTGAAG 1335  
Db 1619 GAGCACTGCTGAAG 1633

RESULT 5  
BD235872  
LOCUS BD235872 2699 bp DNA linear PAT 17-JUL-2003  
DEFINITION Isolated DNA encoding human H3 histamine receptor.  
ACCESSION BD235872  
VERSION BD235872.1 GI:33045642  
KEYWORDS JP 2002526049-A/5.  
SOURCE synthetic construct  
ORGANISM other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 2699)  
AUTHORS Labenberg,T.W., Erlander,M., Huber,A. and Platei,J.  
TITLE Isolated DNA encoding human H3 histamine receptor  
JOURNAL Patent: JP 2002526049-A 5 20-AUG-2002;  
ORWHO MCNEIL PHARMACEUTICAL INC  
COMMENT OS Artificial Sequence  
PN JP 2002526049-A/5  
PD 20-AUG-2002  
PF 07-OCT-1998 JP 2000573370  
PI TIMOTHY W LABENBERG, MARK ERLANDER, ARNE HUBER, JIYAYASYURY PI  
PIATEI  
PC C12N15/09, A61K38/00, A61K45/00, A61P3/04, A61P3/10, A61P9/06, PC  
A61P25/16,  
PC A61P25/18, A61P25/22, A61P25/24, A61P25/28, C07K14/705, C07K16/28,  
PC C12N1/15,  
PC C12N1/19, C12N1/21, C12N5/10, C12P21/02, C12Q1/02, C12Q1/68 PC  
GOIN33/15, GOIN33/50,  
PC C12N15/00, A61K37/02, C12N5/00  
CC Description of Artificial Sequence: CDNA  
FH Key Location/Qualifiers  
FT source 1..2699  
FT /organism='Artificial Sequence'.  
FEATURES  
source  
1..2699  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"

ORIGIN

Query Match 100.0%; Score 1335; DB 6; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 6.7e-178;  
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAGCGCGCGCGCGCGCGCGCTGAACGCTTCGGGGCGCTGGCGGGCGATCGG 60  
Db ATGGAGCGCGCGCGCGCGCGCGCTGAACGCTTCGGGGCGCTGGCGGGCGATCGG 358  
QY 61 GCGGCGCGCGCGCGCGCGCGCTTCGCGCAGCGCTGGACCGCGGTGCTGCGCGCGCTC 120  
Db GCGGCGCGCGCGCGCGCGCGCTTCGCGCAGCGCTGGACCGCGGTGCTGCGCGCGCTC 418  
QY 121 ATGGCGCTGCTCATGCTGGCAGCGGTGCTGGGCAACGCGGTGCTGCTGCTGCTGCTG 180  
Db ATGGCGCTGCTCATGCTGGCAGCGGTGCTGGGCAACGCGGTGCTGCTGCTGCTGCTGCTG 478  
QY 181 GCCGACTCGAGCTCCGCGACCCAGAACAACTTCCTGCTGCTCAACCTCGCCATCTCCGAC 240  
Db GCCGACTCGAGCTCCGCGACCCAGAACAACTTCCTGCTGCTCAACCTCGCCATCTCCGAC 538  
QY 241 TTCTCTGCTGCGCGCTTCCTGATCCCACTGATGATGATGATGATGATGATGATGATGATG 300  
Db TTCTCTGCTGCGCGCTTCCTGATCCCACTGATGATGATGATGATGATGATGATGATGATG 598  
QY 301 ACCTTCGCGCGCGCGCTCTGCAAGCTGTGGTGGTAGTGGACTACTCTGTGCACTCC 360  
Db ACCTTCGCGCGCGCGCTCTGCAAGCTGTGGTGGTAGTGGACTACTCTGTGCACTCC 658

[illegible]





```
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGCTGGGCAACGCGCTGGTCACTGTCGCCCTTCGTG 180
Db 419 ATGGCGCTGCTCATCGTGGCCACGCTGCTGGGCAACGCGCTGGTCACTGTCGCCCTTCGTG 478
QY 181 GCCGACTCGAGGCTCCGACCCAGAACCAACTTCTTCTGCTCAAACTCGCCATCTCCGAC 240
Db 479 GCCGACTCGAGGCTCCGACCCAGAACCAACTTCTTCTGCTCAAACTCGCCATCTCCGAC 538
QY 241 TTCCTGCTGGGCGCTTCTGCAATCCCACTGATGATGATGATGATGATGATGATGATGATG 300
Db 539 TTCCTGCTGGGCGCTTCTGCAATCCCACTGATGATGATGATGATGATGATGATGATGATG 598
QY 301 ACCTTCGCGCGGGGCTCTGCAAGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
Db 599 ACCTTCGCGCGGGGCTCTGCAAGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 658
QY 361 TCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 659 TCTGCTTCAACATCGTCTCATAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 718
QY 421 TCATACCGGGCCAGAGGCTGACACGGCGGGGAGTGCGGAAAGATGCTGCTGCTGCTGCTG 480
Db 719 TCATACCGGGCCAGAGGCTGACACGGCGGGGAGTGCGGAAAGATGCTGCTGCTGCTGCTG 778
QY 481 GTGCTGGCTTCTGCTGACGACCGACGATCTGAGCTGGGAGTACCTGCTGCGGGGGC 540
Db 779 GTGCTGGCTTCTGCTGACGACCGACGATCTGAGCTGGGAGTACCTGCTGCGGGGGC 838
QY 541 AGCTCCATCCCGAGGGGCACTGCTATGCGAGTCTTCTTCAAACTGGTACTTCTCATC 600
Db 839 AGCTCCATCCCGAGGGGCACTGCTATGCGAGTCTTCTTCAAACTGGTACTTCTCATC 898
QY 601 AGGCTTCAACCTGGAGTCTTTAGCGCTTCTTCAAGCTCCTTCAAGCTCCTTCAAGCTCAGC 660
Db 899 AGGCTTCAACCTGGAGTCTTTAGCGCTTCTTCAAGCTCCTTCAAGCTCCTTCAAGCTCAGC 958
QY 661 ATCTACCTGACATCCAGAGGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 959 ATCTACCTGACATCCAGAGGCGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1018
QY 721 GGGCCGAGGCGGCTCCGAGGCGGAGGCGCTCAGGAGGCGGAGGCGGAGGCGGAGGCGGAG 780
Db 1019 GGGCCGAGGCGGCTCCGAGGCGGAGGCGCTCAGGAGGCGGAGGCGGAGGCGGAGGCGGAG 1078
QY 781 TGCTGGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 840
Db 1079 TGCTGGGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 1138
QY 841 GCGGTAGGCGCTGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 900
Db 1139 GCGGTAGGCGCTGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 1198
QY 901 GCTTCAACCCAGCTCCGAGGCTCCGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 960
Db 1199 GCTTCAACCCAGCTCCGAGGCTCCGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCG 1258
QY 961 AAGAGGGGCTCAAGCGCTGCGGCTGCTGCGGCTGCTGCGGAGGAGGAGGAGGAGGAGGAG 1020
Db 1259 AAGAGGGGCTCAAGCGCTGCGGCTGCTGCGGCTGCTGCGGAGGAGGAGGAGGAGGAGGAG 1318
QY 1021 TCCGAGGCTTCAAGCGGCTTCCGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
Db 1319 TCCGAGGCTTCAAGCGGCTTCCGCTGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1378
QY 1081 GCGGTATGCTGAGGAGCTTTTGGGCTGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1140
Db 1379 GCGGTATGCTGAGGAGCTTTTGGGCTGCTGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1438
QY 1141 GGGGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
Db 1439 GGGGCGGCTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1498
```

```
QY 1201 CTGTGGGCAACTCGGCTGTCAACCCCTGTCTTACCTCTGTGTGCGACACAGCTTCCGC 1260
Db 1499 CTGTGGGCAACTCGGCTGTCAACCCCTGTCTTACCTCTGTGTGCGACACAGCTTCCGC 1558
QY 1261 CGGCGCTTACCAAGCTGCTCTGCCCCCAGAGGCTCAAAATCCAGCCCCACAGCTTCCCTG 1320
Db 1559 CGGCGCTTACCAAGCTGCTCTGCCCCCAGAGGCTCAAAATCCAGCCCCACAGCTTCCCTG 1618
QY 1321 GAGCACTGCTGGAAG 1335
Db 1619 GAGCACTGCTGGAAG 1633

RESULT 9
AF321910 1338 bp mRNA linear PRI 24-MAY-2002
LOCUS Homo sapiens histamine H3 receptor isoform 1 (HRH3) mRNA, complete
DEFINITION cds, alternatively spliced.
ACCESSION AF321910
VERSION AF321910.1 GI:18461380
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1338)
AUTHORS Wellendorph, P., Goodman, M.W., Burstein, E.S., Nash, N.R., Brann, M.R.
and Weiner, D.M.
TITLE Molecular Cloning and Characterization of Functionally Distinct
Isoforms of the Human Histamine H3 Receptor
JOURNAL Neuropharmacology (2002) In press
AUTHORS 2 (bases 1 to 1338)
Wellendorph, P., Goodman, M.W., Burstein, E.S., Nash, N.R., Brann, M.R.
and Weiner, D.M.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2000) Target Validation, ACADIA Pharmaceuticals,
3911 Sorrento Valley Blvd., San Diego, CA 92121, USA
FEATURES
source
1..1338
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="hippocampus"
gene 1..1338
/gene="HRH3"
CDS 1..1338
/gene="HRH3"
/feature="alternatively spliced"
/codon_start=1
/product="histamine H3 receptor isoform 1"
/protein_id="AAL7191.1"
/db_xref="GI:18461381"
variation
66
/gene="HRH3"
/feature="polymorphism"
/replace="c"
ORIGIN
Query Match 99.9%; Score 1333.4; DB 9; Length 1338;
Best Local Similarity 99.9%; Pred No. 13e-177;
Matches 1334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
Db 1 ATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 60
```

```
QY 61 GCGGCGGCGGCGGCGGCGGCTTCTCGGAGAGCTGGAACGCGGCTGCTGGCCGCGCTC 120
Db 61 GCGGCGGCGGCGGCGGCGGCTTCTCGGAGAGCTGGAACGCGGCTGCTGGCCGCGCTC 120
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGCTGGGCAACGCGCTGCTGATGCTGCGCTTCG 180
Db 121 ATGGCGCTGCTCATCGTGGCCACGCTGCTGGGCAACGCGCTGCTGATGCTGCGCTTCG 180
QY 181 GCCGACTCGAGGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240
Db 181 GCCGACTCGAGGCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240
QY 241 TTCCTGCTGCGGCGCTTCTGATCCCACTGATGATGATGATGATGATGATGATGATGAT 300
Db 241 TTCCTGCTGCGGCGCTTCTGATCCCACTGATGATGATGATGATGATGATGATGATGAT 300
QY 301 ACCTTCGCGCGGCGCTCTGCAAGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 ACCTTCGCGCGGCGCTCTGCAAGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 TCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCT 420
Db 361 TCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 TCATACCGGCGGCGGCTGACGCGGCGGCGGCTGCGGAGATGCTGCTGCTGCTGCTGCT 480
Db 421 TCATACCGGCGGCGGCTGACGCGGCGGCGGCTGCGGAGATGCTGCTGCTGCTGCTGCT 480
QY 481 GTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 GTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 AGCTCCATCCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 AGCTCCATCCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 ACGGCTTCCACCTCGAGTCTTCTTACGCGCTTCTTACGCGCTTCTTACGCGCTTCTTAC 660
Db 601 ACGGCTTCCACCTCGAGTCTTCTTACGCGCTTCTTACGCGCTTCTTACGCGCTTCTTAC 660
QY 661 ATCTACTGAAATCCAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 661 ATCTACTGAAATCCAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
QY 721 GCGCCGAGCGGCTTCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 GCGCCGAGCGGCTTCCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
QY 781 TGCTGGCAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 781 TGCTGGCAGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
QY 841 GCGTAGGCGGCTGAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 GCGTAGGCGGCTGAGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 GCTTACCCACCTCGAGCTCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 901 GCTTACCCACCTCGAGCTCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 961 AAGAGGCGGCTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 961 AAGAGGCGGCTCAAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1021 TCCAGAGCTTCAACCGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 1021 TCCAGAGCTTCAACCGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 GCGCTCATGCTGAGCATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
Db 1081 GCGCTCATGCTGAGCATCTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
```

```
QY 1141 CCGGCGGCTGCCATGGCCACTGGCTCCCTGACTACTGTTAGTAACTCTTCTTGGCTC 1200
Db 1141 CCGGCGGCTGCCATGGCCACTGGCTCCCTGACTACTGTTAGTAACTCTTCTTGGCTC 1200
QY 1201 CTGTGGGCAACTCGGCTGTCAACCTGCTCTACCTCTGTTGTCACACAGCTTCCGC 1260
Db 1201 CTGTGGGCAACTCGGCTGTCAACCTGCTCTACCTCTGTTGTCACACAGCTTCCGC 1260
QY 1261 CCGGCTTTCACAAAGCTCTGTGCCCCCAGAGCTCAAAATCCAGCCCAAGCTCCCTG 1320
Db 1261 CCGGCTTTCACAAAGCTCTGTGCCCCCAGAGCTCAAAATCCAGCCCAAGCTCCCTG 1320
QY 1321 GAGCACTGCTGGAAG 1335
Db 1321 GAGCACTGCTGGAAG 1335

RESULT 10
AB019000 Homo sapiens mRNA for G-protein coupled receptor, complete cds.
LOCUS AB019000
DEFINITION AB019000
ACCESSION AB019000
VERSION AB019000.1 GI:11022652
KEYWORDS G-protein coupled receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (sites)
Itadani,H., Takimura,T. and Ohta,M.
AUTHORS Itadani,H., Takimura,T. and Ohta,M.
TITLE Novel G-protein coupled receptor
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1362)
AUTHORS Takimura,T., Itadani,H. and Ohta,M.
TITLE Direct Submission
JOURNAL Submitted (20-OCT-1998) Tetsuo Takimura, Banyu Pharmaceutical
Co.,Ltd, Tsukuba Research Institute, Okubo 3, Tsukuba, Ibaraki
300-2611, Japan (E-mail: takimura@banyu.co.jp,
Tel:+81-298-77-2000(ex.2251), Fax:+81-298-77-2027)
FEATURES
Location/Qualifiers
1..1362
source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue type="hypothalamus and hippocampus"
/note="I-103: derived from hypothalamus, 104-1362: derived
from hippocampus"
1..1362
/codon_start=1
/product="G-protein coupled receptor"
/protein_id="BAB17030.1"
/db_xref="GI:11022653"
/translation="MERAPPDPLNAGSALAGEAAGARGFSAATVLAALMALL
IVATVGNALVMAFVADSDRTQNNFLNLAIISDFLGAFCLPLYVPYVITGRTW
GRGLCKLWLVYLLCTSSAFNIVLISYDFLSVTRAVSAQDQDTRAVRKMLLVW
VLAKLCPAILLSWEILSGSSIPEGHCAFFYNWFLITASTLEFPTPLSLVFFN
LSIYLTQRTLRDLGAREAAPEPPAPQSPPPPGCWGCKWGHEAMPLHRYG
VGEAAVGAAGEATLGAGGGGVSASPTSSSSSSRGTGPRSLKRGSKPSASLE
KRMKVQSQFTQRLSRDRKVAKLAVISIFGLCWAPYLLMIIRACHCHCVPDY
WYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKLIKQPHSSLSUEHCWKWKK
TCL"

Query Match 99.8%; Score 1332.4; DB 9; Length 1362;
Best Local Similarity 99.9%; Pred. No. 1.8e-177;
Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGAGCGCGCGCGCGCGCGCTGAAACGCTTCGCGGCGCGCTGCGCGCGCGATGCG 60
Db 1 ATGAGAGCGCGCGCGCGCGCGCTGAAACGCTTCGCGGCGCGCTGCGCGCGCGAGGCG 60
QY 61 CGCGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTCGAGCCGCGGTGTCGCGCGCTC 120
```

Db 61 GCGGGCGGGCGGGCGCGCGCTTCTCGCAGCTGGACCGCGTGTGTCGCCCGCTC 120  
QY 121 ATGGCGCTGCTCATGTCGGCAGCGTGTGGGCAAGCGGTGCTATGCTGCCTTCGTG 180  
Db 121 ATGGCGCTGCTCATGTCGGCAGCGTGTGGGCAAGCGGTGCTATGCTGCCTTCGTG 180  
QY 181 GCCGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 240  
Db 181 GCCGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 240  
QY 241 TTCCTGTGCGCGCTTCTGCAATCCCATGTAATGACCTACGTCGACAGCGCGCTGG 300  
Db 241 TTCCTGTGCGCGCTTCTGCAATCCCATGTAATGACCTACGTCGACAGCGCGCTGG 300  
QY 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTGCTGTGACCTCC 360  
Db 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACTGCTGTGACCTCC 360  
QY 361 TCTGCTTCAACATCGTGTCTCATGACTACGACCGCTTCTGCTGCTCAACCGAGCGTC 420  
Db 361 TCTGCTTCAACATCGTGTCTCATGACTACGACCGCTTCTGCTGCTCAACCGAGCGTC 420  
QY 421 TCATACCGGGCCAGCAGGTGACACGGCGGGCAGTCCGGAAGATGCTGCTGTGTGG 480  
Db 421 TCATACCGGGCCAGCAGGTGACACGGCGGGCAGTCCGGAAGATGCTGCTGTGTGG 480  
QY 481 GTGCTGGCTTCTGCTGTACGACACGACATCTGAGTGGAGTACTGTCGGGGGC 540  
Db 481 GTGCTGGCTTCTGCTGTACGACACGACATCTGAGTGGAGTACTGTCGGGGGC 540  
QY 541 AGCTCATCTCCCGAGGCGCACTGCTATGCCGAGTCTTCTACACTGGTACTTCTCATC 600  
Db 541 AGCTCATCTCCCGAGGCGCACTGCTATGCCGAGTCTTCTACACTGGTACTTCTCATC 600  
QY 601 ACGGCTTCCACCTCGAGTCTTTTACGCTTCTTCCAGCGTCACTTCTTTAACTCAGC 660  
Db 601 ACGGCTTCCACCTCGAGTCTTTTACGCTTCTTCCAGCGTCACTTCTTTAACTCAGC 660  
QY 661 ATCTACTGAAATCCAGAGGGCGACCGCTTCCGGCTGGATGGGCTCGAGAGCAGCC 720  
Db 661 ATCTACTGAAATCCAGAGGGCGACCGCTTCCGGCTGGATGGGCTCGAGAGCAGCC 720  
QY 721 GSCCCGAGCCCTCCGAGGCGCAGCGCTCACCACCCCGCTGGCTGGCTGGGGC 780  
Db 721 GSCCCGAGCCCTCCGAGGCGCAGCGCTCACCACCCCGCTGGCTGGCTGGGGC 780  
QY 781 TGCTGGCAGAGGGCAGCGGAGGCCATGCCGCTGCACAGGTATGGGTGAGGCG 840  
Db 781 TGCTGGCAGAGGGCAGCGGAGGCCATGCCGCTGCACAGGTATGGGTGAGGCG 840  
QY 841 GCGTAGGGCTGAGCCGGGAGGAGCCCTCGGGGTGGCGTGGGGCGGCTCCGTG 900  
Db 841 GCGTAGGGCTGAGCCGGGAGGAGCCCTCGGGGTGGCGTGGGGCGGCTCCGTG 900  
QY 901 GCTTACCCACCTTCAGCTCCGAGCTCTCGAGGGCAGCTGAGAGCCGCTCACTC 960  
Db 901 GCTTACCCACCTTCAGCTCCGAGCTCTCGAGGGCAGCTGAGAGCCGCTCACTC 960  
QY 961 AAGAGGGGTCCAAGCGCTCGCGCTCTCGGCTCGCTGGAGAGCGATGAAGTGGT 1020  
Db 961 AAGAGGGGTCCAAGCGCTCGCGCTCTCGGCTCGCTGGAGAGCGATGAAGTGGT 1020  
QY 1021 TCCGAGAGTTTACCCAGGCTTTTGGCTGTCTCGGACAGGAAAGTGCCGCTG 1080  
Db 1021 TCCGAGAGTTTACCCAGGCTTTTGGCTGTCTCGGACAGGAAAGTGCCGCTG 1080  
QY 1081 GCGTCATCGTAGCATCTTTGGGCTGTGCTGGGCCCCATACACGCTGATGATCATC 1140  
Db 1081 GCGTCATCGTAGCATCTTTGGGCTGTGCTGGGCCCCATACACGCTGATGATCATC 1140  
QY 1141 CGGGCGGCTGCCATGGCCACTGCGTCCCTGACTACTGTTAGCAAACTCTTCTGGCTC 1200  
Db 1141 CGGGCGGCTGCCATGGCCACTGCGTCCCTGACTACTGTTAGCAAACTCTTCTGGCTC 1200

QY 1201 CTGTGGGCAAACTCGGCTGTCAACCCCTGCTCTTACCTCTGTGTCACACAGCTTCGCG 1260  
Db 1201 CTGTGGGCAAACTCGGCTGTCAACCCCTGCTCTTACCTCTGTGTCACACAGCTTCGCG 1260  
QY 1261 CGGGCTTTACCAAGCTGCTCTGCCCCCAGAAAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320  
Db 1261 CGGGCTTTACCAAGCTGCTCTGCCCCCAGAAAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320  
QY 1321 GAGCACTGCTGGAA 1334  
Db 1321 GAGCACTGCTGGAA 1334  
RESULT 11  
E39824  
LOCUS Novel guanosine triphosphate (GTP)-binding protein-conjugate  
DEFINITION E39824 2050 bp DNA linear PAT 31-JAN-2002  
receptor protein.  
ACCESSION E39824  
VERSION E39824.1 GI:18627105  
KEYWORDS JP 2000189171-A/19.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2050)  
AUTHORS Itaya,K., Takimura,T., Nakamura,T., Kobayashi,M., Tana,K.,  
Hidaka,Y. and Ota,M.  
TITLE Novel guanosine triphosphate (GTP)-binding protein-conjugate  
JOURNAL BANYU PHARMACEUT CO LTD  
COMMENT OS Homo sapiens (human)  
PN JP 2000189171-A/19  
PD 11-JUL-2000  
PF 25-MAY-1999 JP 1999145661  
PR 25-DEC-1998 WO PCTJP9805967  
PI KEI ITAYA,TETSUO TAKIMURA,TAKAO NAKAMURA,MASAHICO KOBAYASHI,  
PI KENICHI TANAKA,  
PI YUSUKE HIDAKA,MASAKI OTA  
PC C12N15/09,A61K45/00,C07K14/705,C12N1/15,C12N1/19,C12N1/21, PC  
C12N5/10,  
PC C12P21/02,C12Q1/02,G01N33/15,G01N33/566,C12N15/00,C12N5/00 CC

FEATURES  
source  
FH Key Location/Qualifiers  
FT CDS (271)..(1629).  
1..2050  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 99.8%; Score 1332.4; DB 6; Length 2050;  
Best Local Similarity 99.9%; Pred. No. 1.6e-177;  
Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAGCGCGCGCGCGCGCGCTGAAACCGCTCGGGGCGCTCGGGGCGATGCG 60  
Db 271 ATGAGCGCGCGCGCGCGCGCTGAAACCGCTCGGGGCGCTCGGGGCGAGGCG 330  
QY 61 GCGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGGACCGGGTCTGCGCGGCTC 120  
Db 331 GCGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGGACCGCGGTCTGGCGCGCTC 390  
QY 121 ATGGCGTGTCTCATGTCGGCCACCGTGTGGGCAACGGCTGGTCTGCTCCCTTCGTG 180  
Db 391 ATGGCGTGTCTCATGTCGGCCACCGTGTGGGCAACGGCTGGTCTGCTCCCTTCGTG 450  
QY 181 GCCGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240  
Db 451 GCCGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 510

241 TTCTCTGTCGGCGCCCTTCTGCAATCCCACTGTATGTACCCCTACCTGCTGACAGCCCGCTGG 300  
Db |||||  
511 TTCTCTGTCGGCGCCCTTCTGCAATCCCACTGTATGTACCCCTACCTGCTGACAGCCCGCTGG 570  
Qy  
301 ACCTTCGGCGCGCGCTCTGCAAGCTGTGGCTGTGTAGTGAGTACTGCTGTGTGCACTTCC 360  
Db |||||  
571 ACCTTCGGCGCGCGCTCTGCAAGCTGTGGCTGTGTAGTGAGTACTGCTGTGTGCACTTCC 630  
Qy  
361 TCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTGCTGTGCTACCCGAGCGGTC 420  
Db |||||  
631 TCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTGCTGTGCTACCCGAGCGGTC 690  
Qy  
421 TCATACCGGGCCAGCAGGGTGACACGCGCGGGGACGTGCGGAAGATGCTGTGTGTGG 480  
Db |||||  
691 TCATACCGGGCCAGCAGGGTGACACGCGCGGGGACGTGCGGAAGATGCTGTGTGTGG 750  
Qy  
481 GTGCTGGCTTCTGCTGTACCGGACAGCCATCTGTGAGCTGGAGTACTGTCGGGGGC 540  
Db |||||  
751 GTGCTGGCTTCTGCTGTACCGGACAGCCATCTGTGAGCTGGAGTACTGTCGGGGGC 810  
Qy  
541 AGCTCATCCCCGAGGCGCACTGTATGCGGAGTCTTCTACAACTGGTACTTCTCTCATC 600  
Db |||||  
811 AGCTCATCCCCGAGGCGCACTGTATGCGGAGTCTTCTACAACTGGTACTTCTCTCATC 870  
Qy  
601 ACGGCTTCCACCTGGAGTCTTTTACGCCCTTCTCAGCGTCACTTCTTTAACTCTCAGC 660  
Db |||||  
871 ACGGCTTCCACCTGGAGTCTTTTACGCCCTTCTCAGCGTCACTTCTTTAACTCTCAGC 930  
Qy  
661 ATCTACCTGAACATCCAGAGGCGCACCGCCCTCGGCTGGATGGGCTCGAGAGCAGCC 720  
Db |||||  
931 ATCTACCTGAACATCCAGAGGCGCACCGCCCTCGGCTGGATGGGCTCGAGAGCAGCC 990  
Qy  
721 GGGCCGAGCCCTCCCGAGGCGCACCGCCCTCACCACCCACCGCTGGCTGGGCG 780  
Db |||||  
991 GGGCCGAGCCCTCCCGAGGCGCACCGCCCTCACCACCCACCGCTGGCTGGGCG 1050  
Qy  
781 TGCTGGCAGAGGGGCGCAGGGAGGCGCATGCGGCTGCGACAGGTATGGGTGGGTGAGGCG 840  
Db |||||  
1051 TGCTGGCAGAGGGGCGCAGGGAGGCGCATGCGGCTGCGACAGGTATGGGTGGGTGAGGCG 1110  
Qy  
841 GCGGTAGGGCTGAGGCGGGGAGGAGGACCTTCGGGGGTGGGCTGGGCGCGGCTCCGTC 900  
Db |||||  
1111 GCGGTAGGGCTGAGGCGGGGAGGAGGACCTTCGGGGGTGGGCTGGGCGCGGCTCCGTC 1170  
Qy  
901 GCTTACCCACCTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960  
Db |||||  
1171 GCTTACCCACCTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 1230  
Qy  
961 AAGAGGGGCTCAAGCGGTCGGGCTCTCGGCTCGCTGGAGAGCGCATGAAGATGGTG 1020  
Db |||||  
1231 AAGAGGGGCTCAAGCGGTCGGGCTCTCGGCTCGCTGGAGAGCGCATGAAGATGGTG 1290  
Qy  
1021 TCCAGAGGTTTACCCAGGCTTTCGGCTGTCTCGGAGCAGGAAAGTGCCGCTCGTC 1080  
Db |||||  
1291 TCCAGAGGTTTACCCAGGCTTTCGGCTGTCTCGGAGCAGGAAAGTGCCGCTCGTC 1350  
Qy  
1081 GCGGTATCTGTCAGCATCTTTGGGCTCTGCTGGGCGCCATACACGCTGTGATGATCATC 1140  
Db |||||  
1351 GCGGTATCTGTCAGCATCTTTGGGCTCTGCTGGGCGCCATACACGCTGTGATGATCATC 1410  
Qy  
1141 CGGGCGGCTCGCATGGCCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200  
Db |||||  
1411 CGGGCGGCTCGCATGGCCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1470  
Qy  
1201 CTGTGGGCAACTCGGCTGTCAACCTGCTCTTACCTCTGTGTGCAACACAGCTTCCGC 1260  
Db |||||  
1471 CTGTGGGCAACTCGGCTGTCAACCTGCTCTTACCTCTGTGTGCAACACAGCTTCCGC 1530  
Qy  
1261 CGGGCTTTCACCAAGCTCTGTGCGGCGGAGCTCAAAATCCAGGCGCCACAGCTCCCTG 1320  
Db |||||  
1531 CGGGCTTTCACCAAGCTCTGTGCGGCGGAGCTCAAAATCCAGGCGCCACAGCTCCCTG 1590

Qy 1321 GAGCACTGCTGGAA 1334  
Db 1591 GAGCACTGCTGGAA 1604

RESULT 12  
AR559688  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
ORIGIN

Sequence 21 from patent US 6750322.  
AR559688.1 GI:53969744  
Unknown.  
Unclassified.  
1 (bases 1 to 2050)  
Itadani,H., Takimura,T., Nakamura,T., Kobayashi,M., Tanaka,K.-I.,  
Hidaka,Y. and Ono,M.  
Guanosine triphosphate (GTP) binding protein-coupled receptor  
proteins  
Patent: US 6750322-A 21 15-JUN-2004;  
Location/Qualifiers  
1..2050  
/organism="unknown"  
/mol\_type="genomic DNA"

Query Match 99.8%; Score 1332.4; DB 6; Length 2050;  
Best Local Similarity 99.9%; Pred. No. 1.6e-177;  
Matches 1333; Conservative. 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGGAGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCTGCGGGCGATGCG 60  
Db 271 ATGGAGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCTGCGGGCGAGGCG 330  
Qy 61 GCGGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGAGACCGCGGTGCTGCGCGGCTC 120  
Db 331 GCGGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGAGACCGCGGTGCTGCGCGGCTC 390  
Qy 121 ATGGCGCTGCTCATCGTGGCCACCGTGTGGGCAACGCTGTGCTGCTCACTGCTGCTGCTG 180  
Db 391 ATGGCGCTGCTCATCGTGGCCACCGTGTGGGCAACGCTGTGCTGCTGCTGCTGCTGCTG 450  
Qy 181 GCCGACTCGAGCTCCGCGACCGGCAACCTTCTTCTGCTCAACTGCTGCTGCTGCTGCTGCTG 240  
Db 451 GCCGACTCGAGCTCCGCGACCGGCAACCTTCTTCTGCTCAACTGCTGCTGCTGCTGCTGCTG 510  
Qy 241 TTCTCTGTCGGCGCTTCTGCAATCCCACTGTATGTATGCTGCTGCTGCTGCTGCTGCTGCTG 300  
Db 511 TTCTCTGTCGGCGCTTCTGCAATCCCACTGTATGTATGCTGCTGCTGCTGCTGCTGCTGCTG 570  
Qy 301 ACCTTCGGCGCGCGCTCTGCAAGCTGTGGCTGTGTGAGTACTGCTGTGCACTTCC 360  
Db 571 ACCTTCGGCGCGCGCTCTGCAAGCTGTGGCTGTGTGAGTACTGCTGTGCACTTCC 630  
Qy 361 TCTGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
Db 631 TCTGCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 690  
Qy 421 TCATACCGGGCCAGCAGGGTGACACGCGGGGCGAGTGTGCGGAAGATGCTGTGTGTGG 480  
Db 691 TCATACCGGGCCAGCAGGGTGACACGCGGGGCGAGTGTGCGGAAGATGCTGTGTGTGG 750  
Qy 481 GTGCTGGCTTCTGCTGTACGACCGGCGGCTGCTGAGCTGGGAGTACTGTCGGGGGC 540  
Db 751 GTGCTGGCTTCTGCTGTACGACCGGCGGCTGCTGAGCTGGGAGTACTGTCGGGGGC 810  
Qy 541 AGCTTCATCCCCGAGGCGCACTGTATGCGGAGTCTTCTTCTACAACTGGTACTTCTCTCATC 600  
Db 811 AGCTTCATCCCCGAGGCGCACTGTATGCGGAGTCTTCTTCTACAACTGGTACTTCTCTCATC 870  
Qy 601 ACGGCTTCCACCTGGAGTCTTTTACGCCCTTCTTCTCAGCGTCACTTCTTTAACTCTCAGC 660  
Db |||||

Db 871 ACGGCTTCCACCCCTGGAGTCTTTTACGCCCTTCTCAGCGTCACCTTCTTTAACTCAGC 930  
QY 661 ATCTACCTGAAATCCAGAGGCGCACCCGCTCCGGCTGGATGGGCTCGAGAGCAGCC 720  
Db 931 ATCTACCTGAAATCCAGAGGCGCACCCGCTCCGGCTGGATGGGCTCGAGAGCAGCC 990  
QY 721 GCGCCCGAGCCCTCCGAGGCGCCAGCCCTCACCACCCCGCTGGCTGGCTGGGCG 780  
Db 991 GCGCCCGAGCCCTCCGAGGCGCCAGCCCTCACCACCCCGCTGGCTGGCTGGGCG 1050  
QY 781 TGCTGGCAGAGGCGCAGGAGGCGCATGCGCTGCACAGTATGGGTGGGTGAGGCG 840  
Db 1051 TGCTGGCAGAGGCGCAGGAGGCGCATGCGCTGCACAGTATGGGTGGGTGAGGCG 1110  
QY 841 GCGGTAGCGCTGAGCGGCGGAGCGACCTCGGGGCTGGCGGTGGGCGCGCTCCGTC 900  
Db 1111 GCGGTAGCGCTGAGCGGCGGAGCGACCTCGGGGCTGGCGGTGGGCGCGCTCCGTC 1170  
QY 901 GCTTCAACCCACCTCCAGCTCCGCGCAGCTCCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960  
Db 1171 GCTTCAACCCACCTCCAGCTCCGCGCAGCTCCTCGAGGGGCACTGAGAGGCGCGCTCACTC 1230  
QY 961 AAGAGGGGCTCAAGCCGCTCGCGCTCGCGCTCGTGGAGAGCGCATGAAGATGGT 1020  
Db 1231 AAGAGGGGCTCAAGCCGCTCGCGCTCGCGCTCGTGGAGAGCGCATGAAGATGGT 1290  
QY 1021 TCCGAGGCTTCAACCCAGGCTTTCGGCTGTCTCGGACAGAAAGTGGCCAGTCGCTG 1080  
Db 1291 TCCGAGGCTTCAACCCAGGCTTTCGGCTGTCTCGGACAGAAAGTGGCCAGTCGCTG 1350  
QY 1081 GCGGTATCGTGAGCATCTTTGGGCTCTGCTGGGCGCCATACACGCTGCTGATGATCATC 1140  
Db 1351 GCGGTATCGTGAGCATCTTTGGGCTCTGCTGGGCGCCATACACGCTGCTGATGATCATC 1410  
QY 1141 CGGGCGGCTGCCATGGGCACTGCGTCCGCTACTGCTAGCAAACTCTTCTGGCTC 1200  
Db 1411 CGGGCGGCTGCCATGGGCACTGCGTCCGCTACTGCTAGCAAACTCTTCTGGCTC 1470  
QY 1201 CTGTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTTACCTCTGTGGCACCAGCTTCGCG 1260  
Db 1471 CTGTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTTACCTCTGTGGCACCAGCTTCGCG 1530  
QY 1261 CGGGCTTCAACCAAGTGTCTGCGCCCGAGAGCTCAAAATCCAGCCCGCACAGCTCCCGT 1320  
Db 1531 CGGGCTTCAACCAAGTGTCTGCGCCCGAGAGCTCAAAATCCAGCCCGCACAGCTCCCGT 1590  
QY 1321 GAGCACTGCTGGAA 1334  
Db 1591 GAGCACTGCTGGAA 1604

## RESULT 13

AB045369  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AB045369 2050 bp mRNA linear PRI 23-JAN-2001  
Homo sapiens mRNA for histamine H3 receptor HH3R, complete cds.  
AB045369.1 GI:12248409  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (sites)  
Nakamura, T., Itadani, H., Hidaka, Y., Ohta, M. and Tanaka, K.  
Molecular cloning and characterization of a new human histamine  
receptor, HH4R  
Biochem. Biophys. Res. Commun. 279 (2), 615-620 (2000)  
MEDLINE  
PUBMED  
20568725  
11118334  
2 (bases 1 to 2050)  
Itadani, H.  
Direct Submission  
TITLE  
Submitted (30-JUN-2000) Hiraku Itadani, Banyu Pharmaceutical

Co., Ltd., Biomedical Laboratories; Okubo 3, Tsukuba, Ibaraki  
300-2611, Japan (E-mail: itadani@banyu.co.jp, Tel: 81-298-77-2000,  
Fax: 81-298-77-2027)  
FEATURES  
source  
Location/Qualifiers  
1..2050  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
271..1632  
/codon\_start=1  
/product="histamine H3 receptor HH3R"  
/protein\_id="BAB20090.1"  
/db\_xref="GI:12248410"  
/translation="MERAPDGPGLNASGALAGEAAGARGFSAWTAVALMAL  
IVATVLGNALVLAFAVDASLRTQNNPFLNLAI SDFLVGAFCLPLYVPVYLTRWTF  
GRGKLMVVDYLLTSSAFNI VLIISYDFLSVTRAVSQAQDTRARRAKMLVW  
VLAFLFLGPAIRLDSWEYLSGSSSIPEGHQAQFFYNNWFLITASTLEFFPLSVFFN  
LSIYLNQRTLRDLGAREAGPEPPPEAQSPPPPGCGKMGKSGHEAMPASHRYG  
VGEAAVGAEGEATLGGGGGGSVASPTSSSSSSSRGTERPSRLKRGSKPSSASSLE  
KEMVMSQFTQRFELSPDRKVAKSLAVISI FGLCWAAPYLLMIIRACHGCVDPY  
WYETSFLLMANSVNPVLYPLCHHSFRRAFTKLLCPQKLIKIPHSSLSLEHCWKMKK  
TCL"

## ORIGIN

Query Match 99.8%; Score 1332.4; DB 9; Length 2050;  
Best Local Similarity 99.9%; Pred. No. 1.6e-177;  
Matches 1333; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 ATGAGAGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGGCGCTGCGGGCGATCGG 60  
Db 271 ATGAGAGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGGCGCTGCGGGCGAGCG 330  
QY 61 GCGGCGGCGGCGGCGGCGGCTTCTCGGAGCGCTGAGCGGGTCTGCGCGCGCTC 120  
Db 331 GCGGCGGCGGCGGCGGCGGCTTCTCGGAGCGCTGAGCGGGTCTGCGCGCGCTC 390  
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGTGGCAACGCTGGTCACTGCTGCCCTTCGTG 180  
Db 391 ATGGCGCTGCTCATCGTGGCCACGCTGTGGCAACGCTGGTCACTGCTGCCCTTCGTG 450  
QY 181 GCCGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 240  
Db 451 GCCGACTCGAGCCTCCGACCCAGAACAACTTCTTCTGCTCAACCTGCCATCTCCGAC 510  
QY 241 TTCTCTGTCGCGGCTTCTGATCCCACTGTATGACCTAGCTGCTGACAGCGCGCTGG 300  
Db 511 TTCTCTGTCGCGGCTTCTGATCCCACTGTATGACCTAGCTGCTGACAGCGCGCTGG 570  
QY 301 ACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACTCC 360  
Db 571 ACCTTCGCGCGGCGCTCTGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACTCC 530  
QY 361 TCTGCTTCAACATGCTGCTCATCAGCTACGACCGCTTCTTCTGCTGCTGCTGCTGCTG 420  
Db 631 TCTGCTTCAACATGCTGCTCATCAGCTACGACCGCTTCTTCTGCTGCTGCTGCTGCTG 690  
QY 421 TCATACCGGCGCGGCGGCTGACACGCGGCGGCGAGTGGCGGAGATGCTGCTGCTGCTG 480  
Db 691 TCATACCGGCGCGGCGGCTGACACGCGGCGGCGAGTGGCGGAGATGCTGCTGCTGCTG 750  
QY 481 GTGCTGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 751 GTGCTGGCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 810  
QY 541 AGCTCCATCCCGAGGCGCACTGCTATCCGAGTCTTCTTCTCAACTGGTACTTCTCTCATC 600  
Db 811 AGCTCCATCCCGAGGCGCACTGCTATCCGAGTCTTCTTCTCAACTGGTACTTCTCTCATC 870  
QY 601 ACGGCTTCCACCTGGAGTCTTCTTACGCGCTTCTTACAGCTCACCTTCTTAACTCAGC 660  
Db 871 ACGGCTTCCACCTGGAGTCTTCTTACGCGCTTCTTACAGCTCACCTTCTTAACTCAGC 930  
QY 661 ATCTACCTGAACATCCAGAGGCGCACCGCGCTCGGCTGGATGGGCTCGAGAGGCGAGCC 720



[illegible]



Db 1261 CGGGCCTTCACCAAGCTGCTGTGCCCCCAGAGAAGCTCAAAATCCAGCCCCCAGAGTCCCTG 1320

Qy 1321 GAGCACTGCTGGAAG 1335

Db 1321 GAGCACTGCTGGAAG 1335

Search completed: June 2, 2005, 10:53:04  
Job time : 5782.82 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 04:43:59 ; Search time 712.507 Seconds  
(without alignments)

11091.610 Million cell updates/sec

Title: US-10-727-021-6

Perfect score: 1335

Sequence: 1 atggagcgcgcgcgcgcga.....ccctggagcactgctggaag 1335

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2001bs:\*
- 6: Geneseq2002as:\*
- 7: Geneseq2002bs:\*
- 8: Geneseq2003as:\*
- 9: Geneseq2003bs:\*
- 10: Geneseq2003cs:\*
- 11: Geneseq2003ds:\*
- 12: Geneseq2004as:\*
- 13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1335	100.0	1335	3	AAA09062 Human his
2	1335	100.0	1335	4	AAC62366 cDNA enco
3	1335	100.0	1335	9	ACC59395 Human his
4	1335	100.0	1335	10	ADD22861 Human his
5	1335	100.0	1335	13	ADR31457 Human his
6	1335	100.0	2699	3	AAA09061 Human his
7	1335	100.0	2699	4	AAC62365 Complete
8	1335	100.0	2699	6	ABN84882 Human his
9	1335	100.0	2699	8	ABZ42533 Human his
10	1335	100.0	2699	9	ACC59394 Human his
11	1335	100.0	2699	10	ADD22860 Human ful
12	1335	100.0	2699	13	ADQ89179 Human uro
13	1335	100.0	2699	13	ADR31456 Human his
14	1333.4	99.9	1338	12	ADO29966 Human GPC
15	1332.4	99.8	2050	2	AAH44572 Human G-p
16	1332.4	99.8	2050	3	AAH70637 Human G-p
17	1331.8	99.8	1335	2	AAH70639 Human mAC
18	1331.8	99.8	1401	9	AAH59976 Human w1
19	1331.8	99.8	2689	2	AAH02885 Human mAC
20	1331.8	99.8	2689	2	AAH59167 Human G p

21	1331.8	99.8	2689	2	AAH44572 Human mus
22	1331.8	99.8	2689	8	ABX11852 Human CDN
23	1330.8	99.7	1334	2	AAH44573 Human mus
24	1320.8	98.9	2576	5	AAS76867 DNA enco
25	1237.8	92.7	1359	9	AAH59978 Human H3
26	1206.6	90.4	1293	9	AAH59982 Human H3
27	1152.4	86.3	2145	5	AAS76868 DNA enco
28	1141.8	85.5	1311	9	AAH59979 Human H3
29	1124.4	84.2	2173	6	AAH59983 Human H3
30	1112.6	83.3	1251	9	AAH59983 Human H3
31	1069.2	80.1	1338	2	AAH44575 Rat musca
32	1069.2	80.1	1953	3	AAH70638 Rat G-pro
33	1069.2	80.1	2483	12	ADO30256 Mouse GPC
34	1069.2	80.1	2761	10	ABT42301 Toxicity
35	1069.2	80.1	3244	2	AAH59168 Rat G pro
36	1069.2	80.1	3244	2	AAH44574 Rat musca
37	1069.2	80.1	3244	8	ABX11853 Rat CDNA
38	1067.6	80.0	1338	12	ADF68834 Murine hi
39	1067.6	80.0	18105	8	ABZ82337 Mouse his
40	1016.6	76.1	1203	9	AAH59985 Human H3
41	919.8	68.9	1893	2	AAH59168 Rat G pro
42	919.8	68.9	1893	3	AAH70648 Human G-p
43	899.2	67.4	1239	2	AAH84570 G-protein
44	899.2	67.4	1239	3	AAH70639 Rat G-pro
45	899.2	67.4	2700	3	AAH70640 Rat G-pro

#### ALIGNMENTS

#### RESULT 1

AAA09062

ID AAA09062 standard; CDNA; 1335 BP.

AC AAA09062;

DT 10-AUG-2000 (first entry)

XX Human histamine H3 receptor open reading frame.

XX histamine H3 receptor; biogenic amine receptor homologue; ss.

XX Homo sapiens.

PN WO200020011-A1.

XX 13-APR-2000.

PF 07-OCT-1998; 98WO-US021090.

PR 07-OCT-1998; 98WO-US021090.

PA (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg TW, Erlander M, Huvar A, Pyati J;

DR WPI: 2000-303632/26.

XX P-PSDB; AAY92218.

PT Novel human histamine H3 receptor polynucleotides and polypeptides used in methods to identify modulators of receptor activity.

PS Claim 2; Fig 2; 54pp; English.

XX The cDNA encodes the human histamine H3 receptor. The polypeptide contains the seven conserved hydrophobic domains and specific residues conserved in biogenic amine receptors. The human histamine H3 receptor polynucleotides and polypeptides are used in methods to screen for modulators of receptor activity (claimed). Such agonists and antagonists may prove useful as research tools or may be used as therapeutics to treat disorders directly or indirectly involving histamine receptors (claimed). The characterization of the polynucleotide is useful for forensic analysis, diagnostic applications, and epidemiological studies

XX	SQ	Sequence	1335 BP; 192 A; 476 C; 416 G; 251 T; 0 U; 0 Other;
		Query Match	100.0%; Score 1335; DB 3; Length 1335;
		Best Local Similarity	100.0%; Pred. No. 3.3e-217;
		Matches 1335; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	ATGAGCGCGCGCCGACGGGCCCTGAACGCCTTCGGGGCGCTGGCGGCGATGCG	60
Db	1	ATGAGCGCGCGCCGACGGGCCCTGAACGCCTTCGGGGCGCTGGCGGCGATGCG	60
Qy	61	GCGCGCGCGCGCGCGCGCGGTTCCTCGCAGCCTTGAAACCGCGTGTGCGCGCGCTC	120
Db	61	GCGCGCGCGCGCGCGCGCGGTTCCTCGCAGCCTTGAAACCGCGTGTGCGCGCGCTC	120
Qy	121	ATGCGCGTGTCACTGCGGGCACGGTCTCGGCAACCGCGTGTGCTAAGCTTCGCTCG	180
Db	121	ATGCGCGTGTCACTGCGGGCACGGTCTCGGCAACCGCGTGTGCTAAGCTTCGCTCG	180
Qy	181	GCGACTCGAGCCTCCGACCAGAACAACTTTCTTCGCTCAACCTCGCATCTCCGAC	240
Db	181	GCGACTCGAGCCTCCGACCAGAACAACTTTCTTCGCTCAACCTCGCATCTCCGAC	240
Qy	241	TTCCTCGTGGCGCTTCTGATACCCAATGTAATACCTACGTCGTGACAGCGCGCTGG	300
Db	241	TTCCTCGTGGCGCTTCTGATACCCAATGTAATACCTACGTCGTGACAGCGCGCTGG	300
Qy	301	ACCTTCGCGCGGGCCCTCTCAAGCTGTGCTGTAGTAGACTACCTGCTGTGCACCTCC	360
Db	301	ACCTTCGCGCGGGCCCTCTCAAGCTGTGCTGTAGTAGACTACCTGCTGTGCACCTCC	360
Qy	361	TCTGCCCTTCAACATCGTCTCATCAGCTACGACCGCTTCCTGCTCGGTCAACCGAGCGGTC	420
Db	361	TCTGCCCTTCAACATCGTCTCATCAGCTACGACCGCTTCCTGCTCGGTCAACCGAGCGGTC	420
Qy	421	TCATACCGGCCCCAGCAGGGTGACACCGCGCGGACAGTCGCGAAGATGCTGCTGGTGG	480
Db	421	TCATACCGGCCCCAGCAGGGTGACACCGCGCGGACAGTCGCGAAGATGCTGCTGGTGG	480
Qy	481	GTGCTGCGCTTCCTGCTGACGACACGACCATCTGAGCTGGAGTACCTGTCGGGGGC	540
Db	481	GTGCTGCGCTTCCTGCTGACGACACGACCATCTGAGCTGGAGTACCTGTCGGGGGC	540
Qy	541	AGCTTCATCCCAGGCGCACTGTATGCGAGTTCTTCTACAACCTGGTACTTCTCTCATC	600
Db	541	AGCTTCATCCCAGGCGCACTGTATGCGAGTTCTTCTACAACCTGGTACTTCTCTCATC	600
Qy	601	ACGCTTCCACCTCGAGTTCTTTACGCCCTTCTCAGCGTCACTTTCTTAACTCAGC	660
Db	601	ACGCTTCCACCTCGAGTTCTTTACGCCCTTCTCAGCGTCACTTTCTTAACTCAGC	660
Qy	661	ATCTACCTGAACATCCAGAGCGACCGCTCGGCTGATGGGCTCGAGAGGCGAC	720
Db	661	ATCTACCTGAACATCCAGAGCGACCGCTCGGCTGATGGGCTCGAGAGGCGAC	720
Qy	721	GGCCCCGAGCCCTCCCGAGGCGGACCGCTCACACCCCGCTGCTGCTGGGGC	780
Db	721	GGCCCCGAGCCCTCCCGAGGCGGACCGCTCACACCCCGCTGCTGCTGGGGC	780
Qy	781	TGCTGGCAGAAGGGGCGACGGGAGGCCATGCCGCTGCACAGGTATGGGTTGGTGGCG	840
Db	781	TGCTGGCAGAAGGGGCGACGGGAGGCCATGCCGCTGCACAGGTATGGGTTGGTGGCG	840
Qy	841	GCGTAGGCGCTGAGGCGGGGAGGACCTTCGGGGTGGCGTGGGGCGGCTCGGTG	900
Db	841	GCGTAGGCGCTGAGGCGGGGAGGACCTTCGGGGTGGCGTGGGGCGGCTCGGTG	900
Qy	901	GCTTCAACCACTCAGCTCGGCGAGTCTCTCGAGGGGCACTGAGAGCGCGCTCACTC	960
Db	901	GCTTCAACCACTCAGCTCGGCGAGTCTCTCGAGGGGCACTGAGAGCGCGCTCACTC	960
Qy	961	AAGAGGGGCTCAAAGCGCTCGGCGTCTCTCGGCTCTCGTGGAGAGCGCATGAAGTGGT	1020













```
RESULT 7
AAC62365
ID AAC62365 standard; cDNA; 2699 BP.
XX
AC AAC62365;
XX
DT 19-MAR-2001 (first entry)
XX
DE Complete nucleotide sequence of cDNA encoding a histamine H3 receptor.
XX
KW Human; histamine H3 receptor; inflammation; allergy; ss.
XX
OS Homo sapiens.
XX
XX US6136559-A.
XX
PD 24-OCT-2000.
XX
XX 07-OCT-1998; 98US-00167354.
XX
XX 07-OCT-1998; 98US-00167354.
XX
PA (ORTH ) ORTHO PHARM CORP.
XX
PI Lovenberg TW, Pyati J, Erlander M, Huvar A;
XX
XX WPI; 2001-023168/03.
XX
XX Novel DNA molecules useful in gene therapy for the treatment of
PT inflammation or allergy, or for encoding a human histamine H3 receptor
PT and identifying histamine receptor modulators that are useful as
PT therapeutic and diagnostic agents.
XX
PS Claim 1; Fig 1A-B; 25pp; English.
XX
CC The present sequence represents the complete sequence of cDNA encoding a
CC human histamine H3 receptor. The histamine H3 receptor DNA molecules are
CC useful for isolating homologues of receptor, identifying and isolating
CC genomic equivalents of receptor, and identifying, detecting or isolating
CC mutant forms of the receptor. The DNA molecules are also useful in gene
CC therapy for the treatment of inflammation or allergies. The human
CC histamine H3 receptor protein is useful in identifying modulators of the
CC human histamine H3 receptor, which in turn are useful as therapeutic and
CC diagnostic agents
XX
SQ Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;
Query Match 100.0%; Score 1335; DB 4; Length 2699;
Best Local Similarity 100.0%; Pred. No. 3.3e-217;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAGCGCGCCCGGACCGGCGCGTGAACGGTTTCGGGGCGCTGCGGGCGATCGG 60
DB 299 ATGGAGCGCGCGCCCGGACCGGCGCGTGAACGGTTTCGGGGCGCTGCGGGCGATGCG 358
QY 61 GCGGCGGCGGCGGCGGCGGCGGCTTCGCGAGCGCTGAGACCGCGGTGCGCGCGCTC 120
DB 359 GCGGCGGCGGCGGCGGCGGCGGCTTCGCGAGCGCTGAGACCGCGGTGCGCGCGCTC 418
QY 121 ATGGCGCTGCTCATCGTGGCCACCGTGTGCGGCAACCGCGCTGCTCATGCTCGCTTCGTG 180
DB 419 ATGGCGCTGCTCATCGTGGCCACCGTGTGCGGCAACCGCGTGTGCTCATGCTCGCTTCGTG 478
QY 181 GCCGACTCGAGCTCCGACCCGACCAACACTTCTTCCTGCTCAACCTCGCCATCTCCGAC 240
DB 479 GCCGACTCGAGCTCCGACCCGACCAACACTTCTTCCTGCTCAACCTCGCCATCTCCGAC 538
QY 241 TTCCTCGTGGCGCTTCGTCATCCACTGATGATCCCTAGCTGCTGACAGCGCGCTGG 300
DB 539 TTCCTCGTGGCGCTTCGTCATCCACTGATGATGATCCCTAGCTGCTGACAGCGCGCTGG 598
QY 301 ACCTTCGGCGGCGCTTCGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACTCC 360
DB 301 ACCTTCGGCGGCGCTTCGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACTCC 360
```

```
DB 599 ACCTTCGGCGGCGCTTCGCAAGCTGTGGCTGGTAGTGGACTACCTGCTGTGCACTCC 658
QY 361 TCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCCTGTCGGTCAACGCGCGCTC 420
DB 659 TCTGCTTCAACATCGTCTCATCAGCTACGACCGCTTCCTGTCGGTCAACGCGCGCTC 718
QY 421 TCATACCGGCGCCAGCAGCGGTGACACGCGGGGCGAGTGCAGAGATGCTGCTGGTGG 480
DB 719 TCATACCGGCGCCAGCAGCGGTGACACGCGGGGCGAGTGCAGAGATGCTGCTGGTGG 778
QY 481 GTGCTGGCTTCTCTGCTGTACGACACGACCATCTCTGAGCTGGGAGTACTCTGTCGGGGGC 540
DB 779 GTGCTGGCTTCTCTGCTGTACGACACGACCATCTCTGAGCTGGGAGTACTCTGTCGGGGGC 838
QY 541 AGCTCCATCCCGAGGGCCACTGTATGCCAGTCTTCTTACAACTGTGCTACTTCTCATC 600
DB 839 AGCTCCATCCCGAGGGCCACTGTATGCCAGTCTTCTTACAACTGTGCTACTTCTCATC 898
QY 601 ACGGCTTCCACCTGGAGTCTTTTACGCGCTTCTCTCAGCGTCACCTTCTTTAACTCAGC 660
DB 899 ACGGCTTCCACCTGGAGTCTTTTACGCGCTTCTCTCAGCGTCACCTTCTTTAACTCAGC 958
QY 661 ATCTACCTGAATCCAGAGGCGCACCGCGCTCCGGCTGGATGGGGCTCGAGAGCAGCC 720
DB 959 ATCTACCTGAATCCAGAGGCGCACCGCGCTCCGGCTGGATGGGGCTCGAGAGCAGCC 1018
QY 721 GGGCCGAGGCCCTTCCCGAGGCGCAGCCCTTACACCCCGCTGGCTGGCTGGGGC 780
DB 1019 GGGCCGAGGCCCTTCCCGAGGCGCAGCCCTTACACCCCGCTGGCTGGCTGGGGC 1078
QY 781 TGCTGGCAGAGAGGCGCAGCGGAGCCATCGCGTGCACAGGTATGGGTGGTGGTGGC 840
DB 1079 TGCTGGCAGAGAGGCGCAGCGGAGCCATCGCGTGCACAGGTATGGGTGGTGGTGGC 1138
QY 841 GCCGTAGCGCTGAGGCGCGGCGAGCGACCTTCGCGGGTGGCGTGGGGCGGCTCCGTG 900
DB 1139 GCCGTAGCGCTGAGGCGCGGCGAGCGACCTTCGCGGGTGGCGTGGGGCGGCTCCGTG 1198
QY 901 GCTTACCCACCTTCAGCTCCGCGAGCTTCTTCGAGGGGCACTGAGAGCGCGGCTCACTC 960
DB 1199 GCTTACCCACCTTCAGCTCCGCGAGCTTCTTCGAGGGGCACTGAGAGCGCGGCTCACTC 1258
QY 961 AAGAGGGGCTCCAGAGCGCTCGCGCTTCCTCGCGCTCGTGGAGAGCGCATGAAGATGGT 1020
DB 1259 AAGAGGGGCTCCAGAGCGCTCGCGCTTCCTCGCGCTCGTGGAGAGCGCATGAAGATGGT 1318
QY 1021 TCCAGAGCTTTCACCCAGCGCTTTTCGGCTGTCTCGGGACAGGAAAGTGCCCAAGTCGTG 1080
DB 1319 TCCAGAGCTTTCACCCAGCGCTTTTCGGCTGTCTCGGGACAGGAAAGTGCCCAAGTCGTG 1378
QY 1081 GCGGTATCGTAGGATCTTTGGGGCTGTGCTGGGGCCCATACACGCTGCTGATGATCATC 1140
DB 1379 GCGGTATCGTAGGATCTTTGGGGCTGTGCTGGGGCCCATACACGCTGCTGATGATCATC 1438
QY 1141 CGGGCGGCTCGCATGGCCACTGCTGCTCCCTGACTACTGTAAGAACTCTTCTTGGGCTC 1200
DB 1439 CGGGCGGCTCGCATGGCCACTGCTGCTCCCTGACTACTGTAAGAACTCTTCTTGGGCTC 1498
QY 1201 CTGTGGGGCAACTCGGCTGTCAACCCCTGCTCTTACCTCTGTGTGTCACACAGCTTCGCG 1260
DB 1499 CTGTGGGGCAACTCGGCTGTCAACCCCTGCTCTTACCTCTGTGTGTCACACAGCTTCGCG 1558
QY 1261 CGGGCTTTCAGAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGCTCCCTG 1320
DB 1559 CGGGCTTTCAGAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGCTCCCTG 1618
QY 1321 GAGCACTGCTGGAAG 1335
DB 1619 GAGCACTGCTGGAAG 1633
RESULT 8
ABN84882
```







Qy	721	GGCCCCGAGCCCTCCCGAGGCCACGCTCACCA	CCCCCA	CCGCTCGCTGCTGTGGGGC	780
Db	1019	GGCCCCGAGCCCTCCCGAGGCCACGCTCACCA	CCCCCA	CCGCTCGCTGCTGTGGGGC	1078
Qy	781	TGCTGGCAGAGGGGACGCGGGAGGCCATGCCGCTGCACAGGATATGGGTGGGTGAGGCG			840
Db	1079	TGCTGGCAGAGGGGACGCGGGAGGCCATGCCGCTGCACAGGATATGGGTGGGTGAGGCG			1138
Qy	841	GCCGTAGCGCTGAGAGCGCGGGAGGCCACCTCGGGGGTGGCGGTGGGGCGGCTCCGCTG			900
Db	1139	GCCGTAGCGCTGAGAGCGCGGGAGGCCACCTCGGGGGTGGCGGTGGGGCGGCTCCGCTG			1198
Qy	901	GCTTACCCCACTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCCCGCGCTCACTC			960
Db	1199	GCTTACCCCACTCCAGCTCCGGCAGCTCTCGAGGGGCACTGAGAGGCCCGCGCTCACTC			1258
Qy	961	AAGAGGGGCTCCAAGCCGTGGCGTCTCGGCTCGCTGGAGAAGCCATGAAGATGGTG			1020
Db	1259	AAGAGGGGCTCCAAGCCGTGGCGTCTCGGCTCGCTGGAGAAGCCATGAAGATGGTG			1318
Qy	1021	TCCCAGAGCTTCAACCAGCGCTTTTCGGCTGTCTCGGACAGGAAAGTGGCCAGTTCGCTG			1080
Db	1319	TCCCAGAGCTTCAACCAGCGCTTTTCGGCTGTCTCGGACAGGAAAGTGGCCAGTTCGCTG			1378
Qy	1081	GCGCTCATCTGTAGCATCTTTTGGGCTCTGTGTGGGCCCCATACACGCTGCATGATCATC			1140
Db	1379	GCGCTCATCTGTAGCATCTTTTGGGCTCTGTGTGGGCCCCATACACGCTGCATGATCATC			1438
Qy	1141	CGGGCCGCTGCGCATGGCCACTCGGTCCCTGACTACTGTGATAGAAACCTCTCTTGTGCTC			1200
Db	1439	CGGGCCGCTGCGCATGGCCACTCGGTCCCTGACTACTGTGATAGAAACCTCTCTTGTGCTC			1498
Qy	1201	CTGTGGGCAACTCGCGTGTCAACCCCTGTCTCTACCTCTGTGTGCCACACAGCTTCCGC			1260
Db	1499	CTGTGTGGGCAACTCGCGTGTCAACCCCTGTCTCTACCTCTGTGTGCCACACAGCTTCCGC			1558
Qy	1261	CGGGCCCTTCAACAGCTGCTCTGCCGCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG			1320
Db	1559	CGGGCCCTTCAACAGCTGCTCTGCCGCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG			1618
Qy	1321	GAGCACTGCTGGAAG	1335		
Db	1619	GAGCACTGCTGGAAG	1633		
RESULT 11					
ID	ADD22860 standard; cDNA; 2699 BP.				
XX	AC ADD22860;				
XX	AC ADD22860;				
DT	15-JAN-2004 (first entry)				
DE	Human full length cDNA encoding histamine H3 receptor.				
KW	Human; ss; Histamine H3 receptor; GPCR; G protein-coupled receptor; gene;				
KW	depression; anxiety; schizophrenia; Parkinson's disease; obesity;				
KW	hypertension; Tourette's syndrome; sexual dysfunction; drug addiction;				
KW	drug abuse; cognitive disorder; Alzheimer's disease;				
KW	obsessive-compulsive behaviour; panic attack; pain; eating disorder;				
KW	anorexia; cardiovascular disorder; cerebrovascular disorder; diabetes;				
KW	constipation; arrhythmia; ulcer; asthma; allergy; inflammation;				
XX	prostate dysfunction.				
OS	Homo sapiens.				
XX	OS				
FX	Key				
FT	CDS				
FT	299..1636				
FT	/*tag= a				
FT	/product= "Histamine H3 receptor"				
XX	PN				
XX	US6437100-B1.				

[illegible]





Db 419 ATGGCGCTCTCATCGTGGCCACCGTGTGGGCAACGGCGTGGTCTCATGCTCGCTTCGTG 478  
Qy 181 GCCGACTCGAGCTCCGACACCCAGAACAACTTCTTCCTGCTCAAGCTCGCCATCCGAC 240  
Db 479 GCCGACTCGAGCTCCGACACCCAGAACAACTTCTTCCTGCTCAAGCTCGCCATCCGAC 538  
Qy 241 TTCCTCGTGGCGCTTCTGCACTCCCACTGTATGTACCTACCTAGCTGTGACAGCGCGCTGG 300  
Db 539 TTCCTCGTGGCGCTTCTGCACTCCCACTGTATGTACCTAGCTGTGACAGCGCGCTGG 598  
Qy 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTAGTGGACTACTCTGTGTGCACTCC 360  
Db 599 ACCTTCGGCGGGGCTCTGCAAGCTGTGGTGTGGTAGTGGACTACTCTGTGTGCACTCC 658  
Qy 361 TCTGCTTTCACATCGTGTCTATCAGCTACGACCGCTTCTGCTCGGTACCCGAGGGTC 420  
Db 659 TCTGCTTTCACATCGTGTCTATCAGCTACGACCGCTTCTGCTCGGTACCCGAGGGTC 718  
Qy 421 TCATACCGGGCCAGCAGGGGTGACACGGCGGGGAGTGCAGAGATGCTGTGTGTGG 480  
Db 719 TCATACCGGGCCAGCAGGGGTGACACGGCGGGGAGTGCAGAGATGCTGTGTGTGG 778  
Qy 481 GTGCTGGCTTCTCTGTGTACGACACGACCATCTGAGCTGGGAGTACTGTCCGGGGC 540  
Db 779 GTGCTGGCTTCTCTGTGTACGACACGACCATCTGAGCTGGGAGTACTGTCCGGGGC 838  
Qy 541 AGCTCATCCCGAGGGCCACTGCTATGCCGAGTTCCTTACAACTGGTACTTCTCATC 600  
Db 839 AGCTCATCCCGAGGGCCACTGCTATGCCGAGTTCCTTACAACTGGTACTTCTCATC 898  
Qy 601 AGGGCTTCCACCTCGAGTTCCTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAGC 660  
Db 899 AGGGCTTCCACCTCGAGTTCCTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAGC 958  
Qy 661 ATCTACCTGAACATCCAGAGGCGCACCGGCTCCGGCTGGATGGGGCTCGAGAGCAGCC 720  
Db 959 ATCTACCTGAACATCCAGAGGCGCACCGGCTCCGGCTGGATGGGGCTCGAGAGCAGCC 1018  
Qy 721 GCGCCGAGCCCTCCGAGGCGCCAGCCCTCACACCCCAACCGCTGGCTGGCTGGGGC 780  
Db 1019 GCGCCGAGCCCTCCGAGGCGCCAGCCCTCACACCCCAACCGCTGGCTGGCTGGGGC 1078  
Qy 781 TGCTGGCAGAGGGGCACGGGAGGCGCATCGCGCTGCACAGGTATGGGGTGGGTGAGGCG 840  
Db 1079 TGCTGGCAGAGGGGCACGGGAGGCGCATCGCGCTGCACAGGTATGGGGTGGGTGAGGCG 1138  
Qy 841 GCGGTAGGCGCTGAGCGCGGGAGGCGACCTTCGGGGTGGCGGTGGGGCGGCTCCGCTG 900  
Db 1139 GCGGTAGGCGCTGAGCGCGGGAGGCGACCTTCGGGGTGGCGGTGGGGCGGCTCCGCTG 1198  
Qy 901 GCTTACCCACCTCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960  
Db 1199 GCTTACCCACCTCAGCTCCGGCAGCTCCTCGAGGGGCACTGAGAGGCGCGCTCACTC 1258  
Qy 961 AAGAGGGGCTCAAGCGCTCGCGCTCCTCGGCTCGCTGGAAGCGCATGAAGTGGT 1020  
Db 1259 AAGAGGGGCTCAAGCGCTCGCGCTCCTCGGCTCGCTGGAAGCGCATGAAGTGGT 1318  
Qy 1021 TCCGAGAGCTTCCAGCGCTTTCGGGTGTCTCGGACAGGAAAGTGCCCAAGTCGCTG 1080  
Db 1319 TCCGAGAGCTTCCAGCGCTTTCGGGTGTCTCGGACAGGAAAGTGCCCAAGTCGCTG 1378  
Qy 1081 GCGCTCATGCTAGCATCTTTGGGCTCTGCTGGGCCCATACAGCTGTGTATGATCATC 1140  
Db 1379 GCGCTCATGCTAGCATCTTTGGGCTCTGCTGGGCCCATACAGCTGTGTATGATCATC 1438  
Qy 1141 CGGGCGGCTCGCATGGCCACTCGCTCGCTCTGCTACTGTGTAGAAACCTCTTCTGGCTC 1200  
Db 1439 CGGGCGGCTCGCATGGCCACTCGCTCGCTCTGCTACTGTGTAGAAACCTCTTCTGGCTC 1498  
Qy 1201 CTGTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTGTGTGCAACACAGCTTCGCG 1260  
Db 1499 CTGTGGGCAACTCGGCTGTCAACCTGTCTTACCTCTGTGTGCAACACAGCTTCGCG 1558

Qy 1261 CGGGCTTCCACCAAGCTCTGTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320  
Db 1559 CGGGCTTCCACCAAGCTCTGTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1618  
Qy 1321 GAGCACTGCTGGAAG 1335  
Db 1619 GAGCACTGCTGGAAG 1633  
RESULT 13  
ADR31456  
ID ADR31456 standard; cDNA; 2699 BP.  
XX ADR31456;  
AC ADR31456;  
XX 04-NOV-2004 (first entry)  
DT Human histamine H3 receptor cDNA #1.  
XX  
DE Human; Parkinson's disease; obesity; Alzheimer's disease; pain; stress;  
KW ulcer; constipation; non-insulin dependent diabetes mellitus; gene; ss;  
KW histamine H3 receptor.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 299..1636  
FT /\*tag= a  
FT /product= "Human histamine H3 receptor protein"  
XX  
PN US2004156845-A1.  
XX  
PD 12-AUG-2004.  
XX  
PF 02-DEC-2003; 2003US-00727021.  
PR 07-OCT-1998; 98US-00167354.  
PR 21-AUG-2000; 2000US-00642852.  
XX  
PA (LOVE/) LOVENBERG T W.  
PA (ERLA/) ERLANDER M.  
PA (HUVA/) HUVAR A.  
PA (PYAT/) PYATI J.  
XX  
PI Lovenberg TW, Erlander M, Huvar A, Pyati J;  
XX  
XX WPI; 2004-592726/57.  
DR P-PSDB; ADR31458.  
XX  
PT Novel isolated and purified human histamine H3 receptor protein useful  
PT for identifying modulators utilized for treating Parkinson's disease,  
PT obesity, Alzheimer's disease, pain, stress or ulcers.  
XX  
PS Claim 2; SEQ ID NO 5; 26pp; English.  
XX  
CC The present invention provides a human histamine H3 receptor protein and  
CC nucleic acid encoding such protein. The invention is useful for  
CC identifying compounds that modulate the activity of human histamine H3  
CC receptor. The invention is useful for treating a condition that is  
CC mediated by a human histamine H3 receptor in a patient and for treating  
CC Parkinson's disease, obesity, Alzheimer's disease, pain, stress, ulcers,  
CC constipation and non-insulin dependent diabetes mellitus. The present  
CC sequence is a human histamine H3 receptor cDNA.  
XX  
SQ Sequence 2699 BP; 404 A; 988 C; 805 G; 502 T; 0 U; 0 Other;  
Query Match 100.0%; Score 1335; DB 13; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 3.3e-217;  
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGGAGCGCGGCCCGCCGACGGCGCTGAAACGCTTCGGGGCGCTGCGGGCGATGCG 60  
|||||



of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia), disorders of the adrenal gland, disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1338 BP; 193 A; 476 C; 418 G; 251 T; 0 U; 0 Other;

Query Match 99.9%; Score 1333.4; DB 12; Length 1338;  
Best Local Similarity 99.9%; Pred. No. 6.1e-217;  
Matches 1334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGCGCGCGCCCGACGCGCGCGCTTGAACGCTTCGGGGCGCTCGCGGGCGATGCG 60  
DB 1 ATGAGCGCGCGCGCCCGACGCGCGCGCTTGAACGCTTCGGGGCGCTCGCGGGCGAGGGG 60

QY 61 GCGGCGGGGGGGGGGGGGGGGGTTCGCGAGCGCTTGAGACCGCGGGTGTGCGCGCGCTC 120  
DB 61 GCGGCGGGGGGGGGGGGGGGGGTTCGCGAGCGCTTGAGACCGCGGGTGTGCGCGCGCTC 120

QY 121 ATGGCGCTGCTCATGCTGGCCAGCGGTGTGGGCAACGGCTGGTATGCTGCCTTCGTT 180  
DB 121 ATGGCGCTGCTCATGCTGGCCAGCGGTGTGGGCAACGGCTGGTATGCTGCCTTCGTT 180

QY 181 GCCGACTCGAGCTCGGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240  
DB 181 GCCGACTCGAGCTCGGACCCAGAACAACTTCTTCTGCTCAACCTCGCCATCTCCGAC 240

QY 241 TTCCTGCTGGCGCTTTCGATCCCACTGTATGATACCTACGCTGACAGCGCGCTGG 300  
DB 241 TTCCTGCTGGCGCTTTCGATCCCACTGTATGATACCTACGCTGACAGCGCGCTGG 300

QY 301 ACCTTCGCGCGGGGCTCTGAAAGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 360  
DB 301 ACCTTCGCGCGGGGCTCTGAAAGCTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 360

QY 361 TCTGCTTCAACATCGTGTCTCATAGCTACGACCGCTTCTTCTGCTCGGTACCCGAGCGGT 420  
DB 361 TCTGCTTCAACATCGTGTCTCATAGCTACGACCGCTTCTTCTGCTCGGTACCCGAGCGGT 420

QY 421 TCATACCGGGCCAGAGGGTGACACGCGCGGGCAGTGCAGAAATGCTGTGTGTGG 480  
DB 421 TCATACCGGGCCAGAGGGTGACACGCGCGGGCAGTGCAGAAATGCTGTGTGTGG 480

QY 481 GTGCTGGCTTCTGCTGTACGACACGACCATCTGAGCTGGAGTACTGTTCGCGGGG 540  
DB 481 GTGCTGGCTTCTGCTGTACGACACGACCATCTGAGCTGGAGTACTGTTCGCGGGG 540

QY 541 AGCTCCATCCCGAGGGCCACTGTATGCCGAGTTCTTCTACAACTGGTACTTCTCTCATC 600

DB 541 AGCTCCATCCCGAGGGCCACTGTATGCCGAGTTCTTCTACAACTGGTACTTCTCTCATC 600  
QY 601 ACGGCTTCCACCTCGAGTTCTTTACGGCTTCTTCTCAGCGTCACTTCTTTAACTCAGC 660  
DB 601 ACGGCTTCCACCTCGAGTTCTTTACGGCTTCTTCTCAGCGTCACTTCTTTAACTCAGC 660  
QY 661 ATCTACCTGAAATCCAGAGCGGACCGGCTTCGGCTGGATGGGCTCGAGAGCGAGCC 720  
DB 661 ATCTACCTGAAATCCAGAGCGGACCGGCTTCGGCTGGATGGGCTCGAGAGCGAGCC 720  
QY 721 GGGCCCGAGCCCTTCCCGAGGCGCCAGCCCTCACACACCCCGCTTGGCTGGGGC 780  
DB 721 GGGCCCGAGCCCTTCCCGAGGCGCCAGCCCTCACACACCCCGCTTGGCTGGGGC 780  
QY 781 TGCTGGCAGAGAGGGGACCGGGAGGCGCATGCGCTGCAAGGTATGGGGTGGGTGAGGG 840  
DB 781 TGCTGGCAGAGAGGGGACCGGGAGGCGCATGCGCTGCAAGGTATGGGGTGGGTGAGGG 840  
QY 841 GCCGTAGCGCTGAGGCGGGGAGGCGGACCTTCGGGGGTGGCGGTGGGGCGGCTCCGTG 900  
DB 841 GCCGTAGCGCTGAGGCGGGGAGGCGGACCTTCGGGGGTGGCGGTGGGGCGGCTCCGTG 900  
QY 901 GCTTCACCCACTCCTCAGCTCCGCGAGCTCCTCGAGGGGCACTGAGAGCGCGCTCACTC 960  
DB 901 GCTTCACCCACTCCTCAGCTCCGCGAGCTCCTCGAGGGGCACTGAGAGCGCGCTCACTC 960  
QY 961 AAGAGGGGCTCAAGCGCTCGGCGTCTCGGCTCGCTGGAGAGCGGATGAAGATGGTG 1020  
DB 961 AAGAGGGGCTCAAGCGCTCGGCGTCTCGGCTCGCTGGAGAGCGGATGAAGATGGTG 1020  
QY 1021 TCCCAGAGCTTCAACCGAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCAAGTCGCTG 1080  
DB 1021 TCCCAGAGCTTCAACCGAGCGCTTTCGGCTGTCTCGGGACAGGAAAGTGGCAAGTCGCTG 1080  
QY 1081 GCCGTATCGTGAAGCATCTTTGGGCTGTGCTGGGCCCCATACACGCTGCTGATGATCATC 1140  
DB 1081 GCCGTATCGTGAAGCATCTTTGGGCTGTGCTGGGCCCCATACACGCTGCTGATGATCATC 1140  
QY 1141 CGGGCGCTCGCATGGGCACTGGTCCCTGACTACTGTAGTAAACCTCTTCTTGGCTC 1200  
DB 1141 CGGGCGCTCGCATGGGCACTGGTCCCTGACTACTGTAGTAAACCTCTTCTTGGCTC 1200  
QY 1201 CTGTGGGCAACTGGGCTGTCAACCTGCTCTTACCTCTGTGTGCAACACAGCTTCGCG 1260  
DB 1201 CTGTGGGCAACTGGGCTGTCAACCTGCTCTTACCTCTGTGTGCAACACAGCTTCGCG 1260  
QY 1261 CGGGCTTTCACCAAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320  
DB 1261 CGGGCTTTCACCAAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320  
QY 1321 GAGCACTGCTGAAG 1335  
DB 1321 GAGCACTGCTGAAG 1335

RESULT 15  
AAK84572 standard; DNA; 2050 BP.  
XX AAK84572;  
XX AC  
XX XX  
DT 14-SEP-1999 (first entry)  
XX  
DE Human G-protein conjugate-type receptor protein coding sequence.  
KW Guanosine triphosphate binding protein; signal transduction regulation;  
KW G-protein conjugate-type receptor protein; learning difficulty; BG2;  
KW muscarinic acetylcholine receptor; physiological function disorder;  
KW blood pressure; digestion; sleep; therapy; human; ss.  
OS Homo sapiens.  
XX  
PN W09933978-A1.



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 05:10:00 ; Search time 4400.8 Seconds  
(without alignments)  
11546.944 Million cell updates/sec

Title: US-10-727-021-6

Perfect score: 1335

Sequence: 1 atggagcgccgcgcgcga.....ccctggagcactgctggaag 1335

Scoring table: IDENTITY NUC

Gapop 10\_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsa1:\*

9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	677	50.7	732	7	CF147822	AGENCOURT
2	541.8	40.6	890	4	BI731453	603354331
3	516	38.7	716	7	CN423054	170004245
4	462.8	34.7	672	6	CB556920	AMGNNUC:U
5	412.6	30.9	910	2	BE783826	601471053
6	390.8	29.3	547	6	CB611519	AMGNNUC:N
7	385.4	28.9	1103	4	BM548665	AGENCOURT
8	371.2	27.8	499	2	BF567596	UT-R-B00-
9	369.6	27.7	519	2	AW669811	113386 MA
10	340.8	25.5	1046	5	BQ950659	AGENCOURT
11	331	24.8	946	5	BQ668856	AGENCOURT
12	294.4	22.1	842	7	CO403631	AGENCOURT
13	277	20.7	653	6	BY727560	BY727560
14	272.8	20.4	434	6	CB758850	AMGNNUC:S
15	264.2	19.8	853	6	CD326085	AGENCOURT
16	240.6	18.0	490	6	CB725716	AMGNNUC:U
17	224.2	16.8	643	3	AL848045	AL848045
18	218	16.3	533	6	CB154982	K-EST0213
19	214.4	16.1	258	2	AW654609	104607 MA
20	212	15.9	484	1	AA859887	UT-R-E0-C
21	208	15.6	538	2	AW654493	103977 MA
22	197.8	14.8	975	9	CNS0399V	Tetraodon
23	189.8	14.2	236	2	BE063702	QV3-BT029
24	180.8	13.5	281	2	BB592940	BB592940

c

#### ALIGNMENTS

RESULT 1  
CF147822  
LOCUS CF147822 732 bp mRNA linear EST 25-JUL-2003  
DEFINITION AGENCOURT\_14740187 NIH\_MGC\_145 Homo sapiens CDNA clone  
IMAGE:6971899 5', mRNA sequence.  
ACCESSION CF147822  
VERSION CF147822.1 GI:33244090  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 732)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: GPCR Consortium  
CDNA Library Preparation: GPCR Consortium  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: IRB102 row: b column: 06  
High quality sequence stop: 610.  
Location/Qualifiers  
1..732  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6971899"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_145"  
/note="Vector: pcDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pcDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clone represents,  
please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearranged\\_plates/IRBI.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRBI.presv.dat)

25 174.4 13.1 775 9 CC580463  
26 173.6 13.0 1440 5 AY404934  
27 173.4 13.0 916 5 BUI47486  
28 172.4 12.9 1440 4 AY404935  
29 172.2 12.9 1048 4 BM805220  
30 171.6 12.9 975 1 AL536991  
31 171.6 12.9 1078 4 BM548382  
32 169.8 12.7 855 6 CB565879  
33 167.6 12.6 650 4 BI064672  
34 166.4 12.5 2410 3 BC035047  
35 165.8 12.4 795 6 CD804122  
36 165.2 12.4 3816 3 AK081248  
37 164.2 12.3 623 7 CV026860  
38 164.2 12.3 812 1 AL537084  
39 164.2 12.3 1108 5 BM907142  
40 162 12.1 952 5 BX355053  
41 161.8 12.1 727 7 CR366545  
42 161.2 12.1 206 2 AW327105  
43 160.2 12.0 1037 9 CNS022VG  
44 159.4 11.9 887 5 BX424634  
45 159.2 11.9 732 7 CK958826

CC580463 CH240\_375  
AY404934 Homo sapi  
BUI47486 AGENCOURT  
AY404935 Pan trogl  
BM805220 AGENCOURT  
AL536991 AL536991  
BM548382 AGENCOURT  
CB565879 AGENCOURT  
BI064672 pgfln.pk0  
BC035047 Homo sapi  
CD804122 UT-M-GVO-  
AK081248 Mus muscu  
CV026860 4931 Full  
AL537084 AL537084  
BM907142 AGENCOURT  
BX355053 BX355053  
CR366545 CR366545  
AW327105 20622 MAR  
AL178693 Tetraodon  
BX424634 BX424634  
CK958826 409592 B





```
QY 1251 CAGCTTCGCGCGGCTTACCAAGCTGCTTGCCCCCAGAGCTCAAAATCCAGCCCCA 1310
Db 657 CAGCTTCGCTAGAGCTTACCAAGCTCTCTGCCCCCAGAGCTCAAGGTCCAGCCCCA 716
QY 1311 CAGCTCCCTGGAGCACTGCTGAAG 1335
Db 717 TGGCTCCCTGGAGCACTGCTGAAG 741

RESULT 3
LOCUS CN423054 716 bp mRNA linear EST 16-MAY-2004
DEFINITION 1700424504731 GRN_ES Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN423054
VERSION CN423054.1 GI:47410648
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 716)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Quesler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
JOURNAL Transcriptome characterization elucidates signaling networks that
COMMENT control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760
Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00.
FEATURES
source
1..716
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN ES"
/note="oligo dt primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match 38.7%; Score 516; DB 7; Length 716;
Best Local Similarity 100.0%; Pred. No. 1e-92;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 250 GCGCGCTTCTGCATCCCACTGATGACCTTACCTAGCTGCTGACAGCGCGTGGACCTTCGCG 309
Db 201 GCGCGCTTCTGCATCCCACTGATGATGACCTTACCTAGCTGCTGACAGCGCGTGGACCTTCGCG 260
QY 310 CGGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACTCTCTGCTTC 369
Db 261 CGGGCGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACTCTCTGCTTC 320
QY 370 AACATCGTGCTCATCAGCTTACGACCGCTTCTCGTTCGGTCCACCGGCGGTCTCATACCGG 429
Db 321 AACATCGTGCTCATCAGCTTACGACCGCTTCTCGTTCGGTCCACCGGCGGTCTCATACCGG 380
QY 430 GCCAGCAGGGTGACACGCGCGGCGAGTGCAGGAAGTCTGCTGTGGGTGTGCGCC 489
Db 381 GCCAGCAGGGTGACACGCGCGGCGAGTGCAGGAAGTCTGCTGTGGGTGTGCGCC 440
QY 490 TTCCTGCTGTACGACCAACCACTCTGAGCTGGGAGTACCTTCCGGGGGAGCTCCATC 549
Db 441 TTCCTGCTGTACGACCAACCACTCTGAGCTGGGAGTACCTTCCGGGGGAGCTCCATC 500
```

```
QY 550 CCCGAGGGCCACTGTATGCGGAGTTCTTTTACAACTGGTACTTCTCTCATACGGCTTCC 609
Db 501 CCCGAGGGCCACTGTATGCGGAGTTCTTTTACAACTGGTACTTCTCTCATACGGCTTCC 560
QY 610 ACCCTGGAGTTCTTTTACAGCCCTTCTCAGCGTCACTCTTTTAACTCAGCATCTACCTG 669
Db 561 ACCCTGGAGTTCTTTTACAGCCCTTCTCAGCGTCACTCTTTTAACTCAGCATCTACCTG 620
QY 670 AACATCCAGAGCGCACCGCCTCCGGGTGGATGGGCTTCGAGAGGACGCCGCCGCGGAG 729
Db 621 AACATCCAGAGCGCACCGCCTCCGGGTGGATGGGCTTCGAGAGGACGCCGCCGCGGAG 680
QY 730 CCCCTCCCGAGGCCAGCCCTTCACACCCCCACCG 765
Db 681 CCCCTCCCGAGGCCAGCCCTTCACACCCCCACCG 716

RESULT 4
LOCUS CB556920 672 bp mRNA linear EST 02-APR-2003
DEFINITION AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone
ACCESSION CB556920 urgp1-00001-d6 5', mRNA sequence.
VERSION CB556920.1 GI:29496320
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 672)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
FEATURES
source
1..672
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urgp1-00001-d6"
/clone_lib="urgp1 (14349)"
/note="Vector: pSPORT1; Rat GPCR library rearranged
internal pSPORT vector"

ORIGIN
Query Match 34.7%; Score 462.8; DB 6; Length 672;
Best Local Similarity 89.7%; Pred. No. 4.2e-82;
Matches 497; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGAGAGCGCGCGCCCGACGCGCGCTTGAAACGCTTCGGGGCGCGTGGCGGCGATGCG 60
Db 119 ATGAGAGCGCGCGCGCCCGACGCGCGCTTGATGAACGCTTCGGGCACTCTGCCGAGAGCG 178
QY 61 GCGGGCGCGCGCGCGCGCGCGCTTCTCGGAGAGCTGAGCCGCGGTGCTGCCCGCGCTC 120
Db 179 GCGGTGAGAGCGCGCGCGCGCTTCTCGGCTGCTGAGACGCTGTCTGCGCTC 238
QY 121 ATGGCGCTGCTCATCGTGGCCACGCTGTGGCAACGCGCTGCTATGCTCGCTTCGCTG 180
Db 239 ATGGCGCTGCTCATCGTGGCCACGCTGTGGCAACGCGCTGCTATGCTCGCTTCGCTG 298
QY 181 GCCGATCAGCCTCCGACCCAGAACAACTTTCTTCTGCTCAACCTGCCATCTCCGAC 240
Db 299 GCGGATTCAGCCTCCGACCCAGAACAACTTTCTTCTGCTCAACCTGCCATCTCCGAC 358
QY 241 TTCCTGCTGCGCGCTTCTGATCCCACTGTATGATCCCTAGCTGTGAGCAGCGCGCTGG 300
Db 359 TTCCTGCTGCGCGCTTCTGATCCCACTGTATGATCCCTAGCTGTGAGCAGCGCGCTGG 418
```

```

QY 301 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTGACTACTCTGTGTGCACTCC 360
Db 419 ACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGGTAGTAGACTACTGTGTGCTCC 478
QY 361 TCTGCTTCAACATCGTGTCTATCAGCTACGACCGCTTCTCTCGGTCAACCGAGCGGTC 420
Db 479 TCGGTCTTCAACATCGTGTCTATCAGCTATGACCGATTCTCTGAGTCACTCGAGCTGTC 538
QY 421 TCATACCGGGCCAGCAGGCTGACAGCGCGCGGCGAGTGGCGAAGATGCTGTGTGTGG 480
Db 539 TCTACAGGGCCAGCAGGCGGACAGACAGCGGGCGGTTTCGAAGATGGCACTGGGTGG 598
QY 481 GTGCTGGCTTCTCTGTGTACGACAGCCATCTCTGAGCTGGAGTACTGTGCGGGGCG 540
Db 599 GTGCTGGCTTCTCTGTGTATGGGCTGCCATCTCTGAGTTGGAGTACCTGTCTGTGGC 658
QY 541 AGCTCCATCCCGA 554
Db 659 AGTTCCATCCCGA 672

RESULT 5
LOCUS BE783826 601471053F1 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:3874260 5',
DEFINITION mRNA sequence.
ACCESSION BE783826
VERSION BE783826.1 GI:10205024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9631 row: i column: 13
High quality sequence stop: 601.
FEATURES
source
1..910
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3874260"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 30.9%; Score 412.6; DB 2; Length 910;
Best Local Similarity 96.9%; Pred. No. 4.6e-72;
Matches 443; Conservative 0; Mismatches 9; Indels 5; Gaps 2;
QY 879 TGGCGGTGGGGCGGCTCGTGGCTTACCCACCTCCAGCTCCGGCAGCTCCTCGAGGG 938
Db 1 TGGCGGTGGGGCGGCTCGTGGCTTACCCACCTCCAGCTCCGGCAGCTCCTCGAGGG 60
QY 939 CACTGAGAGCGCGCTCACTCAAGAGGGGCTCCAAGCGGTCCAGCGGTCTCGGCGCTCGCT 998

```

```

Db 61 CACTGAGAGCGCGCTCACTCAAGAGGGGCTCCAAGCGGTCTCGGCGCTCGCT 120
QY 999 GGAGAAAGCGCATGAAGATGGTGTCCAGAGCTTACCCAGCGCTTTCGGCTGTCTCGGA 1058
Db 121 GGAGAAAGCGCATGAAGATGGTGTCCAGAGCTTACCCAGCGCTTTCGGCTGTCTCGGA 180
QY 1059 CAGGAAGTGGCCAAAGTGGCGCGTCACTGTGAGCATCTTTGGGCTCTGTGGGCGCC 1118
Db 181 CAGGAAGTGGCCAAAGTGGCGCGTCACTGTGAGCATCTTTGGGCTCTGTGGGCGCC 240
QY 1119 ATACACGCTGTGTATGATCATCCGGCGCGCTTGCATCGCCACCTCGTCCCTGACTACTG 1178
Db 241 ATACACGCTGTGTATGATCATCCGGCGCGCTTGCATCGCCACCTCGTCCCTGACTACTG 300
QY 1179 GTACAAACCTCTCTTCTGGCTCTGTGGGCGCACTCGGCTGTCAACCTGTCTCTACCC 1238
Db 301 GTACAAACCTCTCTTCTGGCTCTGTGGGCGCACTCGGCTGTCAACCTGTCTCTACCC 360
QY 1239 TCTGTGCCACACACAGCTTCCGCGCGGCTTCAACCAAGCTGTCTGCGCCCGCAAGCTCAA 1298
Db 361 TCTGTGCCACACAGCTT---CGCGGGCTTCAACCAAGCTG--TCTGCCCGCAAGCTCAA 415
QY 1299 AATCCAGCGCCACACAGCTCCTCTGGAGCACTGTCTGGAAG 1335
Db 416 AATCCAGCGCCACACAGCTCCTCTGGAGCACTGTCTGGAAG 452

RESULT 6
LOCUS CB611519 547 bp mRNA linear EST 07-APR-2003
DEFINITION AMGNNUC:NRHY3-00179-H8-A W Rat hypothalamus (10735) Rattus
ACCESSION CB611519
VERSION CB611519.1 GI:29571407
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
TITLE Rattus.
JOURNAL 1 (bases 1 to 547)
COMMENT Amgen EST Program.
Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00179 row: h column: 8.
FEATURES
source
1..547
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrhy3-00179-h8"
/tissue_type="hypothalamus"
/clone_lib="W Rat hypothalamus (10735)"
/notes="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; W Rat
hypothalamus"
ORIGIN
Query Match 29.3%; Score 390.8; DB 6; Length 547;
Best Local Similarity 85.6%; Pred. No. 1e-67;
Matches 471; Conservative 0; Mismatches 72; Indels 7; Gaps 3;
QY 655 CTCAGCATCTACTGAACATCCAGAGGGCGACCCCGCTCCGGCTGGATGGGCTCGAGAG 714
Db 2 CTCAGCATCTACTGAACATCCAGAGGGCGACCCCGCTCCGGCTGGATGGGCGCTGAG 61
QY 715 GGAGCGCGCGGAGCCCTCTCCGAGCGCCAGCCCTCAACACCCCA---CCGCTGCG 771
Db 62 ---GCTGGCCCAAGAACCCCAAGATGCCAGCCCTCGCCACCTCCAGCTCCCGCCAGC 118

```



## source

```
1. 499
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-B00-agr-c-06-0-UI"
/dev_stage="adult"
/lab_host="DH108 (Life Technologies)"
/clone_lib="UI-R-B00"
/notes="Vector: pVT3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The library
(UI-R-B00) is a subtracted library derived from a mixture
of the following tissues: thalamus, cerebellum,
hypothalamus, medulla, pons, midbrain, cerebral cortex,
corpus striatum and hippocampus. For a detailed
description of the library from which this clone was
derived, please visit our web site at
ratest.eng.uiowa.edu. The subtraction has been previously
described in (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)"
```

## ORIGIN

```
Query Match      27.8%; Score 371.2; DB 2; Length 499;
Best Local Similarity 90.0%; Pred. No. 8.2e-64;
Matches 397; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 250 GCGGCTTCTGATCCACTGATGATACCTAGTGTCTGACAGCGCGTGGACCTTCGGC 309
    |||
Db 59 GGTGCTTCTGATCCCATTTGACGTACCTATGCTGACCGCGCGTTGGACCTTCGGC 118
    |||

QY 310 CCGGGCTCTGCAAGCTGGCTGGTGGAGTACTCTGCTGTCGACCTCTCTGCTTC 369
    |||
Db 119 CCGGGCTCTGCAAGCTGGCTGGTGGAGTACTCTGCTGTCGCTCTCTGCTTC 178
    |||

QY 370 AACATCGTCTCATCAGCTACGACCGCTTCTGTCGGTCAACCGAGCGGTCTCATACCG 429
    |||
Db 179 AACATCGTCTCATCAGCTATGACCGATTCTCTGTCAGTCACTCGAGCTCTCTACAGG 238
    |||

QY 430 GCGCAGCAGGTGACACCGCGCGGCGAGTGGCGAGATGCTGCTGTTGGTGTCTGGCC 489
    |||
Db 239 GCGCAGCAGGTGACACCGCGCGGCGTTCGGAAGATGGCACTGTTGGTGTCTGGCC 298
    |||

QY 490 TTCTGCTCTGACGACACCGATCTGAGCTGGAGTACTCTGTCGGGGGAGCTCCATC 549
    |||
Db 299 TTCTGCTCTGATGGGCTGCCATCTCTGAGTGGAGTACTCTGTTGGTGGAGTCCATC 358
    |||

QY 550 CCGAGGGGCACTGCTATGCGAGTCTTCTTCAACTGGTACTTCTCATCAGCGCTTC 609
    |||
Db 359 CCGAGGGGCACTGCTATGCTGAGTCTTCTTCAACTGGTACTTCTCATCAGCGNCTCC 418
    |||

QY 610 ACCCTGGAGTTCTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAGCATCTACCTG 669
    |||
Db 419 ACCCTGGAGTTCTTACGCGCTTCTCAGCGTCACTTCTTCAACTCAGCATCTACCTG 478
    |||

QY 670 AACATCCAGAGGGCGACCCGC 690
    |||
Db 479 AACATCCAGAGGGCGACCCGC 499
    |||
```

## RESULT 9

```
AW669811      519 bp mRNA linear EST 25-APR-2001
LOCUS 113386 MARC 180V Bos taurus cdna 5', mRNA sequence.
DEFINITION ACCESSION
AW669811
VERSION AW669811.1 GI:7526325
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE 1 (bases 1 to 519)
AUTHORS Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
```

TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithemail.marc.usda.gov  
Single pass sequencing. Bases called and alt\_trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.

PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCTCCAGTCAGCAGC  
Plate: 108 row: H column: 13  
Seq primer: ATTAGGTGACACTATAG.

FEATURES  
source

1. 519  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/tissue\_type="pooled"  
/lab\_host="DH108"  
/clone\_lib="MARC 180V"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
Library made from pooled tissue from lymph node, ovary,  
fat, hypothalamus, and pituitary."

## ORIGIN

```
Query Match      27.7%; Score 369.6; DB 2; Length 519;
Best Local Similarity 84.9%; Pred. No. 1.7e-63;
Matches 440; Conservative 0; Mismatches 69; Indels 9; Gaps 2;

QY 644 CTTCTTTTAACTCAGCATCTACCTGAACATCCAGAGCGCACCCGCTTCGGCTGGATG 703
    |||
Db 2 CTTCTTTTAACTCAGCATCTACCTGAACATCCAGAGCGCACCCGCTTCGGCTGGATG 61
    |||

QY 704 GGGCTCGAGAGCAGCCGCGCGCGCGCTCCCGAGCGCCAGCCCTCACACCC--- 760
    |||
Db 62 GAGTCGCGGAGCAGCACCACCGAGCTTCCACCGAGGCCAGCCCTCTCCACCGCTG 121
    |||

QY 761 CACCGCTTGGCTGCTGGGGCTGCTGGCAGAGGGGACGCGGAGGCGCATGCCGCTGCACA 820
    |||
Db 122 CGGACCCAGCTGCTGGGGATGCTGGCAGAAAGGGTGGGGAGGCGCGCTCGCTGCACA 181
    |||

QY 821 GGTATGGGGTGG- - - - -GTGAGGCGCGCTGAGGCGCTGAGCGCGGGAGGCGACCTCG 874
    |||
Db 182 GGTACGGGGTGGGGGTGACCGAGAGTGACCCAGGCGCTGAGGCGGGAGGTGGCGCTCG 241
    |||

QY 875 GGGGTGGCGGTGGGGCGGCTCCGTTGCTTACCCACCTCAGCTCCGCGACCTCTCTCA 934
    |||
Db 242 GGGGTGGTAGCGGTGGGGGTGCGCGCGCTCCGCCACCTCCAGCTCCGCGACCTCTCTCA 301
    |||

QY 935 GGGGCACTGAGAGGCGCGCTCAGTCAAGAGGGGTCCAAGCGCTCGGCGCTCTCGGCT 994
    |||
Db 302 GGGGCACTGAGAGGCGCTCGCTCAGTCAAGAGGGGTCCAAGCGCTCTCGGCTCTCTAGCT 361
    |||

QY 995 CGCTGGAGAAGCGCATGAAGATGGTGTCTCCAGAGCTTCCACCGAGCGCTTCGGCTGTCTC 1054
    |||
Db 362 CCCTCGAGAAGCGCATGAAGATGGTGTCTCCAGAGCATCACTCATCGCTTCGGCTCTCTC 421
    |||

QY 1055 GGGACAGAAAGTGGCCAGTGGCTGGCGCTCATCTGTAGAGCATCTTGGGCTCTGCTGG 1114
    |||
Db 422 GGGACAAAGAGTAGCAAGTCACTGGCGCTCATCTGTAGAGCATCTTGGGCTCTGCTGG 481
    |||

QY 1115 CCCATACAGCTGCTGATGATCATCCGCGCGCGCTGC 1152
    |||
```

```
|||||
482 CCCCCACACACTCTCTGATGATCATTCGGCGCGCCTGC 519

RESULT 10
BQ950659      1046 bp      mRNA      linear      EST 21-AUG-2002
LOCUS      AGENCOURT_8863943 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311932
DEFINITION  5', mRNA sequence.
ACCESSION  BQ950659
VERSION    BQ950659.1 GI:22366137
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
JOURNAL    NIH-MGC http://mgc.nci.nih.gov/
COMMENT    National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
cDNA Library Preparation: ResGen, Invitrogen Corp
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13736 row: k column: 05
High quality sequence stop: 640.
FEATURES             source
    Location/Qualifiers
        1..1046
            /organism="Mus musculus"
            /mol_type="mRNA"
            /db_xref="taxon:10090"
            /clone="IMAGE:6311932"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH MGC 129"
            /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
            Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.
            Primer: Oligo dr. Average insert size 2.2 kb. Constructed
            by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
            Library."
ORIGIN
Query Match      25.5%; Score 340.8; DB 5; Length 1046;
Best Local Similarity 78.7%; Pred. No. 18-57;
Matches 472; Conservative 0; Mismatches 117; Indels 11; Gaps 5;

QY      240 CTTCTCGTCGGCGCCTTCGCATCCACTGTATGTACCCCTACGCTGCTGACAGCGCGCTG 299
DB      430 CTTTCTATAGTGCTTCTGATCCCATTTGATGTACCTATGTGCTGACCGCGGCTG 489
QY      300 GACCTTGGCCGGGCGCTTCGAAGCTGTGGTGTAGTGGACTACCTGCTGTGACCTTC 359
DB      490 GACCTTGGCCGGGCGCTTCGAAGCTGTGGTGTAGTGGACTACCTGCTGTGCTTC 549
QY      360 CTCCTGCTTCACATCGTCTCATGCTACACCGCTTCCTGTGCTGCTGACCGAGCGGT 419
DB      550 CTCAGTCTTTCACATCGTCTCATGCTACACCGATTCCTGTGCTGCTGCTGCTGCT 609
QY      420 CTCATACCGGGCCACGAGGGTGACACGGCGGGCAGTGGCGGAAGATCTCTGCTGTG 479
DB      610 CTCCTACCGGGCCACGAGGGGACACAGACGGGCTGTTCGGAAGATGGCACTGTGTG 669
QY      480 GGTGCTGGCCTTCTGCTGTACGGACCGACCATCTGAGCTGGGAGTACCTGTCCGGGG 539
DB      670 GGTGCTGGCCTTCTGCTGTATGGGCTTGGCATCTGAGTGGGAGTACCTGTCCGGTG 729
QY      540 CAGCTCCATCCCGAGGGCCATGCTATGCCAGTTTCTTCTACAACCTGTACTTCTCAT 599
DB      730 CAACTCCATCCCGAGGGCCACTGTGATGCTGAGTTCTTCTAC-ACCTGTACTTCTCAT 788
```

---

```
QY      600 CACGGCTTCCACCCCTGGAGTTCTTTACGCGCTTCTCTACGCGTCACCTCTTTAACTCAG 659
DB      789 CACGGGCTCCACACCTCGAGTTCTTCA-ACCTTCTCTAGCGTTACCTTCTCAACCTCAG 847
QY      660 CATCTACTGTACATCCAGAGCGGCAC-CCGCTCGGCTGGATGGGCTCGAGAGGCAG 718
DB      848 CATCTAACTGGAATCCAGAGGGGCACTCTCTTCGTTTATGGGGGCCCAAAAG--G 905
QY      719 CCGGCGCGAGCCCTCCCGAGGGCCAGCCCTCACCACC-----CCACCGCCTGGCT 772
DB      906 CTGGCCCAATAACCCCACTGGAGGCGAAGCTTGGCACCTCAGGTTCCCCACATGGT 965
QY      773 GCTGGGGTGTCTGGCAGAAAGGGGACGGGAGGCGCATGCCGTGCACAGGTATGGGGTGG 832
DB      966 TGGGGGTTCTGTGGCCAATAGGGCGCGCAGACCTGACCTATAACACGGCTGCTGGGGG 1025

RESULT 11
BQ068856
LOCUS      AGENCOURT_6740127 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802702
DEFINITION  5', mRNA sequence.
ACCESSION  BQ068856
VERSION    BQ068856.1 GI:19897902
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
JOURNAL    NIH-MGC http://mgc.nci.nih.gov/.
COMMENT    National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ruben Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2037 row: i column: 07
High quality sequence stop: 678.
FEATURES             source
    Location/Qualifiers
        1..946
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:5802702"
            /tissue_type="neuroblastoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_47"
            /note="Organ: brain; Vector: pORF7; Site 1: XhoI; Site 2:
            EcoRI; cDNA made by oligo-dr priming. Directionally
            cloned into EcoRI/XhoI sites using the following 5',
            adaptor: GGCACGAG(G). Size-selected >500bp for average
            insert size 1.8kb. Library constructed by Ling Hong in
            the laboratory of Gerald M. Rubin (University of
            California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."
ORIGIN
Query Match      24.8%; Score 331; DB 5; Length 946;
Best Local Similarity 100.0%; Pred. No. 9.1e-56;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1005 GGCATGAGATGGTGTCCAGAGCTTCACCCAGCGCTTCGGCTGTCTCGGAGCAGGAA 1064
DB      1 GCGCATGAGATGGTGTCCAGAGCTTCACCCAGCGCTTCGGCTGTCTCGGAGCAGGAA 60
```

QY 1065 AGTGGCCAAAGTGGCTGGCTCATCTGAGCATCTTTGGGCTCTGCTGGGCCCATACAC 1124  
|||||  
Db 61 AGTGGCCAAAGTGGCTGGCTCATCTGAGCATCTTTGGGCTCTGCTGGGCCCATACAC 120  
|||||  
QY 1125 GCTGCTGATGATCATCCGGGGCGCTGCGCATGGCCATCGTCCCTGACTACTGTGTACGA 1184  
|||||  
Db 121 GCTGCTGATGATCATCCGGGGCGCTGCGCATGGCCATCGTCCCTGACTACTGTGTACGA 180  
|||||  
QY 1185 AACCTCTCTGCTGGCTGGGGCAACTCGGCTGTCAACCTGTGCTTACCTCTCTGTG 1244  
|||||  
Db 181 AACCTCTCTGCTGGCTGGGGCAACTCGGCTGTCAACCTGTGCTTACCTCTCTGTG 240  
|||||  
QY 1245 CCACCACAGCTTCCGGCGGGCGCTTACCAAGTGTCTGCCCCCAGAAAGCTCAAAATCCA 1304  
|||||  
Db 241 CCACCACAGCTTCCGGCGGGCGCTTACCAAGTGTCTGCCCCCAGAAAGCTCAAAATCCA 300  
|||||  
QY 1305 GCCCCACAGCTCCCTGGAGCACTGTGTGGAAG 1335  
|||||  
Db 301 GCCCCACAGCTCCCTGGAGCACTGTGTGGAAG 331  
|||||

RESULT 12  
CO403631  
LOCUS  
DEFINITION  
CO403631 842 bp mRNA linear EST 01-JUL-2004  
AGENCOURT 27526928 NIH.MGC.254 Rattus norvegicus cDNA clone  
IMAGE:7315203 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Rattus norvegicus (Norway rat)  
Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE  
1 (bases 1 to 842)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs-remail.nih.gov  
Tissue procurement: Drs. Josef Lazar & Howard Jacob, Medical  
College of Wisconsin

cDNA Library Preparation: Express Genomics  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Place: LLNMI5369 row: b column: 01  
High quality sequence stop: 637.

FEATURES  
source

Location/Qualifiers  
1. 842  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10116"  
/clone="IMAGE:7315203"  
/sex="both"  
/tissue\_type="Brain - Pooled from several tissues from one  
or more individuals"  
/clone\_lib="NIH MGC 254"  
/note="Organ: brain/CNS; Vector: pExpress-1; Site:1:  
ECORV; Site 2: NotI; RNA obtained from brain tissue of 8  
wk old animal. Tissues were snap-frozen and kept at -80C  
before RNA extraction and purification (Tri-reagent  
method). cDNA was primed using oligo-dt primer:  
5'-pGACTGTTCTAGTCGAGCGCGCC(T)25-3' and cloned into  
the pECORV/NotI sites of pExpress-1. Size-selection into  
resulted in an average insert size of 2.18 kb. This  
primary library is not normalized (normalized library is

NIH MGC 255) and was constructed by Express Genomics  
(Frederick, MD). Note: this is a NIH\_MGC library"

## ORIGIN

Query Match 22.1%; Score 294.4; DB 7; Length 842;  
Best Local Similarity 90.7%; Pred. No. 1.8e-48;  
Matches 313; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 1 ATGGAGCGCGCGCGCGCGCGCGCTGAAACGCTTCGGGGCGCTGGCGGCATCGG 60  
|||||  
Db 335 ATGGAGCGCGCGCGCGCGCGCGCTGATGAACGGCTGGGCACACTGTGCCGAGAGGGG 394  
|||||  
QY 61 GCGGCGCGCGCGCGCGCGCGCGCTTCTCGGAGCTCGAACCGCTGTGCGCGCGCTC 120  
|||||  
Db 395 GCGGCTGAGGCGGGCGGGCGGGCTTCTCGGCTGTGACCGCTGTCTGTGGCTGCTC 454  
|||||  
QY 121 ATGGCGCTGCTCATCTGTGGCCACCGTGTGGGCAACGGCTGTGCTCATGCTCGCCTTCGTG 180  
|||||  
Db 455 ATGGCGCTGCTCATCTGTGGCCACAGTACTGTGGCAACGGCTGTGCTCATGCTCGCCTTCGTG 514  
|||||  
QY 181 GCGGACTGAGCTCGGCGCGCGCGCGCGCGCTTCTTCCTGCTCAACCTGCCATCTCCGAC 240  
|||||  
Db 515 GCGGATTCGAGCTCGGCGCGCGCGCGCGCGCTTCTTCCTGCTCAACCTGCCATCTCCGAC 574  
|||||  
QY 241 TTCCTCGTGGCGCGCTTCTGATCCCACTGTATGACCTAGCTGTGACAGCGCGCTGG 300  
|||||  
Db 575 TTCCTCGTGGTGGCTTCTGATACCATGTAGTACCTATGTGCTGACCGCGCTGG 634  
|||||  
QY 301 ACCTTCGCGCGGGCGCTCTGCAAGCTGTGGCTGTGTGGACTAC 345  
|||||  
Db 635 AACTTCGCGGGCGCTCTGCAAGCTGTGGCTGTGTGGTAGACTAC 679  
|||||

## RESULT 13

BY727560

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

BY727560 653 bp mRNA linear EST 17-DEC-2002  
CDNA clone B530005H20 5', mRNA sequence.

BY727560

BY727560.1 GI:27140687

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 653)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojohori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasaki, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Numata, K., Okido, T., Pavan, W.J., Perlea, G., Pesole, G.,

Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Sempile, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,

Verrard, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,

Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,

Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

Arakawa, T., Fukuda, S., Harai, A., Hashizume, W., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shbata, K.,

Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,

Rogers, J., Birney, E. and Hayashizaki, Y.







GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 14:34:44 ; Search time 81 Seconds  
(without alignments)  
2124.795 Million cell updates/sec

Title: US-10-727-021-7

Perfect score: 2361

Sequence: 1 MERAPPDGLNAGSALAGDA.....LLCPQKLIKPHSSLEHCWK 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2361	100.0	445	3	AAY92218	Aay92218 Human his
2	2361	100.0	445	4	AAB30627	Aab30627 A human h
3	2361	100.0	445	5	ABB79792	Abb79792 Human his
4	2361	100.0	445	6	AAO19746	Aao19746 Human his
5	2361	100.0	445	6	ABP81687	Abp81687 Human his
6	2361	100.0	445	6	ABG74567	Abg74567 Human his
7	2361	100.0	445	7	AAO29531	Aao29531 Human wil
8	2361	100.0	445	7	AAO29527	Aao29527 Human wil
9	2361	100.0	445	7	ADD22854	Add22854 Human his
10	2361	100.0	445	8	ADQ089180	Adq089180 Human uro
11	2361	100.0	445	8	ADR31458	Adr31458 Human his
12	2357	99.8	445	2	AAW92975	Aaw92975 Human mac
13	2357	99.8	445	2	AAY06322	Aay06322 Human G p
14	2357	99.8	445	2	AAQ67830	Aaq67830 Human mus
15	2357	99.8	445	6	ABR43667	Abra43667 Human his
16	2357	99.8	445	6	ABP57425	Abp57425 Human his
17	2357	99.8	445	6	ABG76405	Abg76405 Human mus
18	2357	99.8	445	8	ADP66835	Adp66835 Human his
19	2357	99.8	445	8	ADO29494	Ado29494 Human GPC
20	2357	99.8	445	8	ADP76110	Adp76110 Human H3
21	2357	99.8	453	2	AAY22208	Aay22208 Human G-p
22	2357	99.8	453	3	AAI5381	Aai5381 Human G-p
23	2352	99.6	449	4	ABGI2680	Abgi2680 Novel hum
24	2323	98.4	445	6	ABR43668	Abra43668 Monkey hi
25	2323	98.4	445	6	ABP57426	Abp57426 Monkey hi

26	2323	98.4	445	8	ADP76111	Adp76111 Monkey H3
27	2318.5	98.2	714	4	ABGI2681	Abgi2681 Novel hum
28	2266	96.0	431	7	AAO29529	Aao29529 Human H3
29	2320	94.0	445	8	ADF66833	Adf66833 Murine hi
30	2220	94.0	445	8	ADO29495	Ado29495 Mouse GPC
31	2213	93.7	445	2	AAO6323	Aay06323 Rat G pro
32	2213	93.7	445	2	AAQ67831	Aaq67831 Rat musca
33	2213	93.7	445	3	AAI5382	Aai5382 Rat G-pro
34	2213	93.7	445	6	ABR43669	Abra43669 Rat hista
35	2213	93.7	445	6	ABP57427	Abp57427 Rat hista
36	2213	93.7	445	6	ABG76406	Abg76406 Rat musca
37	2213	93.7	445	8	ADP76112	Adp76112 Rat H3 re
38	2156	91.3	409	7	AAO29533	Aao29533 Human H3
39	2146	90.9	415	7	AAO29530	Aao29530 Human H3
40	2061	87.3	395	7	AAO29534	Aao29534 Human H3
41	2057	87.1	413	2	AAI5383	Aay22207 G-protein
42	2057	87.1	413	3	AAI5383	Aai5383 Rat G-pro
43	1941	82.2	379	7	AAO29536	Aao29536 Human H3
44	1919	81.3	365	7	AAO29528	Aao29528 Human H3
45	1915	81.1	365	4	AAQ65580	Aag65580 Human his

ALIGNMENTS

RESULT 1  
AAY92218  
ID AAY92218 standard; protein; 445 AA.

AC AAY92218;

XX XX

DT 10-AUG-2000 (first entry)

DE Human histamine H3 receptor.

XX histamine H3 receptor; biogenic amine receptor homologue.

OS Homo sapiens.

XX WO200020011-A1.

XX PD 13-APR-2000.

XX PF 07-OCT-1998; 98WO-US021090.

XX PR 07-OCT-1998; 98WO-US021090.

XX PA (ORTH ) ORTHO-MCNEIL PHARM INC.

XX PI Lovenberg TW, Erlander M, Huvar A, Pyati J;

XX DR WPI; 2000-303632/26.

XX N-PSDB; AAA09061, AAA09062.

XX Novel human histamine H3 receptor polynucleotides and polypeptides used

XX PT in methods to identify modulators of receptor activity.

XX PS Claim 11; Fig 3; 54pp; English.

XX The human histamine H3 receptor contains the seven conserved hydrophobic  
XX domains and specific residues conserved in biogenic amine receptors. The  
XX human histamine H3 receptor polynucleotides and polypeptides are used in  
XX methods to screen for modulators of receptor activity (claimed). Such  
XX agonists and antagonists may prove useful as research tools or may be  
XX used as therapeutics to treat disorders directly or indirectly involving  
XX histamine receptors (claimed). The characterization of the polynucleotide  
XX is useful for forensic analysis, diagnostic applications, and  
XX epidemiological studies

XX SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 3; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.1e-181;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPDGLNAGSALAGDAAAAGGARGSAATVLAALMALLIVATVGLNALVMLAFV 60  
DB 1 MERAPDGLNAGSALAGDAAAAGGARGSAATVLAALMALLIVATVGLNALVMLAFV 60  
QY 61 ADSSLRTQNNFFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
DB 61 ADSSLRTQNNFFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180  
DB 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180  
QY 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
QY 241 GPEPPEAQPSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300  
DB 241 GPEPPEAQPSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300  
QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFELSRDRKVAKSL 360  
DB 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFELSRDRKVAKSL 360  
QY 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420  
DB 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420  
QY 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445  
DB 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445

## RESULT 2

AAB30627  
ID AAB30627 standard; protein; 445 AA.  
XX  
AC AAB30627;  
XX  
DT 19-MAR-2001 (first entry)  
XX  
DE A human histamine H3 receptor polypeptide.  
XX  
KW Human; histamine H3 receptor; inflammation; allergy.  
XX  
OS Homo sapiens.  
XX  
PN US6136559-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 07-OCT-1998; 98US-00167354.  
XX  
PR 07-OCT-1998; 98US-00167354.  
XX  
PA (ORTH ) ORTHO PHARM CORP.  
XX  
PI Lovenberg TW, Pyati J, Erlander M, Huvar A;  
XX  
DR WPI; 2001-023168/03.  
DR N-PSDB; AAC62366.  
XX  
PT Novel DNA molecules useful in gene therapy for the treatment of  
PT inflammation or allergy, or for encoding a human histamine H3 receptor  
PT and identifying histamine receptor modulators that are useful as  
PT therapeutic and diagnostic agents.  
XX  
PS Example 3; Fig 3; 25pp; English.  
XX  
CC The present sequence represents human histamine H3 receptor. The  
CC histamine H3 receptor DNA molecules are useful for isolating homologues

of receptor, identifying and isolating genomic equivalents of receptor,  
and identifying, detecting or isolating mutant forms of the receptor. The  
DNA molecules are also useful in gene therapy for the treatment of  
inflammation or allergies. The human histamine H3 receptor protein is  
useful in identifying modulators of the human histamine H3 receptor,  
which in turn are useful as therapeutic and diagnostic agents

Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 4; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.1e-181;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPDGLNAGSALAGDAAAAGGARGSAATVLAALMALLIVATVGLNALVMLAFV 60  
DB 1 MERAPDGLNAGSALAGDAAAAGGARGSAATVLAALMALLIVATVGLNALVMLAFV 60  
QY 61 ADSSLRTQNNFFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
DB 61 ADSSLRTQNNFFLLNLAIISDFLVGAFICPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180  
DB 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180  
QY 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFNYWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
QY 241 GPEPPEAQPSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300  
DB 241 GPEPPEAQPSPPPPGCGCKQKGHEAMP LHRVGVGEAAVGAAGATLGGGGGGSV 300  
QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFELSRDRKVAKSL 360  
DB 301 ASPTSSSGSSRGTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFELSRDRKVAKSL 360  
QY 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420  
DB 361 AVISIFGLCWAPYTLMLIIRAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSFR 420  
QY 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445  
DB 421 RAFTKLLCPQKLIKOPHSSLEHCWK 445

## RESULT 3

AAB79792  
ID AAB79792 standard; protein; 445 AA.  
XX  
AC AAB79792;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human histamine H3 receptor.  
XX  
KW Histamine; receptor; G-protein coupled receptor; human. neuroprotective;  
KW cardiant; antidepressant; tranquilizer; antiparkinsonian; anorectic;  
KW hypotensive; analgesic; antidiabetic; laxative; antiarrhythmic; antiulcer;  
KW antiallergic; antiinflammatory.  
XX  
OS Homo sapiens.  
XX  
PN US6413743-B1.  
XX  
PD 02-JUL-2002.  
XX  
PF 21-AUG-2000; 2000US-00642855.  
XX  
PR 07-OCT-1998; 98US-00167354.  
XX  
PA (ORTH ) ORTHO PHARM CORP.

PI	Lovenberg TW, Erlander M, Huvar A, Pyati J;	AAO19746 standard; protein; 445 AA.
XX		
DR	WPI; 2002-641560/69.	AAO19746;
DR	N-PSDB; ABR84882.	
XX		
PT	Novel isolated and purified DNA molecule encoding human histamine H3	11-AUG-2003 (first entry)
PT	receptor protein, useful for identifying modulators of human histamine H3	Human histamine receptor subclass H3 protein.
PT	receptor protein activity.	
XX		
PS	Claim 1; Fig 3; 25pp; English.	Human; histamine receptor; H1; H2; H3; antigen; antibody; antiallergic; antiinflammatory; immunosuppressive; allergy; inflammatory disease.
XX		
CC	The present sequence is the protein sequence of the human histamine H3	Homo sapiens.
CC	receptor, a novel G-protein coupled receptor. The sequence is predicted	
CC	from a cDNA clone isolated from a human thalamus cDNA library. It shows	WO200292634-A2.
CC	at least 25% amino acid identity with the human histamine H2 receptor,	
CC	28% with the human histamine H1 receptor, and approximately 25% with the	21-NOV-2002.
CC	family of biogenic amine G-protein coupled receptors. Histamine H3	
CC	receptor cDNA has been expressed in recombinant host cells, which	
CC	produced active recombinant protein. H3 receptor nucleic acids and	27-APR-2002; 2002WO-EP004678.
CC	proteins can be used to identify modulators of H3 receptor activity or	
CC	expression useful as therapeutic or diagnostic agents for central nervous	27-APR-2001; 2001DE-01020816.
CC	system disorders, such as depression, anxiety, psychoses (e.g.	28-MAR-2002; 2002DE-01013916.
CC	schizophrenia), tardive dyskinesia, Parkinson's disease, obesity,	(SCHA/) SCHAEFER U.
CC	hypertension, Tourette's syndrome, sexual dysfunction, drug addiction,	
CC	drug abuse, cognitive disorders, Alzheimer's disease, senile dementia,	XX Schaefer U, Falus A;
CC	obsessive-compulsive behaviour, panic attacks, pain, social phobias,	PI
CC	eating disorders and anorexia, cardiovascular and cerebrovascular	XX
CC	disorders, non-insulin dependent diabetes mellitus, hyperglycaemia,	DR
CC	constipation, arrhythmia, disorders of the neuroendocrine system, stress	XX
CC	and spasticity, as well as acid secretion, ulcers, airway constriction,	PT
CC	asthma, allergy, inflammation and prostate dysfunction	PT
XX		
SQ	Sequence 445 AA;	Claim 2; Fig 2; 39pp; German.
	Query Match 100.0%; Score 2361; DB 5; Length 445;	
	Best Local Similarity 100.0%; Pred. No. 3.1e-181;	
	Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MERAPDGPLNAGALAGDAAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60	1 MERAPDGPLNAGALAGDAAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60
DB	1 MERAPDGPLNAGALAGDAAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60	
QY	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB	61 ADSSLRTQNNPFLNLALISDFLVGAFICPLIYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120	
QY	121 SAFNIVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180	121 SAFNIVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180
DB	121 SAFNIVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180	
QY	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240
DB	181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNQRTRLRLDGAREAA 240	
QY	241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300	241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300
DB	241 GPEPPEAQSPPPPPGCGWKQKGHEAMP LHR YGVGEAAVGA BAGEATLGGGGGGSV 300	
QY	301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFRLSDRDKVAKSL 360	301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFRLSDRDKVAKSL 360
DB	301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFRLSDRDKVAKSL 360	
QY	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420
DB	361 AVIVSIFGLCWAPYTLMLIIIRAAACHGCVDPDYWYETSFWLLWANSVNPVLPCHHSFR 420	
QY	421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445	
DB	421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445	

QY 421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445  
DB 421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445

## RESULT 5

ABP81687  
ID ABP81687 standard; protein; 445 AA.

XX AC ABP81687;

XX DT 04-MAR-2003 (first entry)

XX DE Human histamine H3 receptor protein SEQ ID NO:549.

XX KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
KW immunological-related cell proliferative disease; autoimmune disease;  
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
KW ulcer.

XX OS Homo sapiens.

XX PN WO200261087-A2.

XX PD 08-AUG-2002.

XX PF 19-DEC-2001; 2001WO-US050107.

XX PR 19-DEC-2000; 2000US-0257144P.

XX PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX PI Burner GC, Roush CL, Brown JP;

XX DR WPI: 2003-046718/04.

XX DR N-PSDB; AB242533.

XX PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
PT autoimmune diseases.  
XX PS Disclosure; Fig 1; 523pp; English.

XX CC The present invention describes antigenic peptides (I) comprising: (a)  
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
CC acids. Also described: (1) an assay for the detection of a particular G  
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
CC and (2) an isolated antibody having high specificity and high affinity or  
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
CC antibody against a particular GPCR, and in the production of specific  
CC antibodies. The peptides and antibodies are also useful for detecting the  
CC presence or absence of corresponding GPCRs. The antigenic peptides for  
CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
CC treating immune-related diseases, growth-related diseases, cell  
CC regeneration-related disease, immunological-related cell proliferative  
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be  
CC used in immunoassays and immunodiagnosis. AB242523 to AB242969 encode  
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
CC exemplification of the present invention

XX SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 6; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.1e-181; Indels 0; Gaps 0;  
Matches 445; Conservative 0; Mismatches 0

QY 1 MERAPPDGLNAGSAGALAGDAAAAGGARGFSAWTAVALAALMALLIVATVIGNALVWLAFV 60

DB 1 MERAPPDGLNAGSAGALAGDAAAAGGARGFSAWTAVALAALMALLIVATVIGNALVWLAFV 60

QY 61 ADSSLRTQNNFFLLNLAIISDFLVGAFCLPLVVPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120

DB 61 ADSSLRTQNNFFLLNLAIISDFLVGAFCLPLVVPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120

QY 121 SAFNIVLISYDRFLSVTRAVSYRAOQGTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180

DB 121 SAFNIVLISYDRFLSVTRAVSYRAOQGTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180

QY 181 SSIPGHCYAEFFYNNWYFLITASTLTLEFPTPLSVTFNLSIYLNIOQTTRLRLDGAARAA 240

DB 181 SSIPGHCYAEFFYNNWYFLITASTLTLEFPTPLSVTFNLSIYLNIOQTTRLRLDGAARAA 240

QY 241 GPEPPPEAQSPPPPPGCGWQKQHGSEAMPRLHRYGVGEAAVGAAGBATLGGGGGGGGSV 300

DB 241 GPEPPPEAQSPPPPPGCGWQKQHGSEAMPRLHRYGVGEAAVGAAGBATLGGGGGGGGSV 300

QY 301 ASPTSSSSSSRGTERPSRLKRGSKPSASASLEKRMKMWVSQSFTORFLSRDRKVKAKSL 360

DB 301 ASPTSSSSSSRGTERPSRLKRGSKPSASASLEKRMKMWVSQSFTORFLSRDRKVKAKSL 360

QY 361 AVIVSIFGLCWAPYTLMLIIRAAACHGCVDPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420

DB 361 AVIVSIFGLCWAPYTLMLIIRAAACHGCVDPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420

QY 421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445

DB 421 RAFTKLLCPQKLIKIQPHSSLEHCWK 445

## RESULT 6

ABG74567

ID ABG74567 standard; protein; 445 AA.

XX AC ABG74567;

XX DT 08-MAY-2003 (first entry)

XX DE Human histamine receptor H3 protein.

XX KW Human; histamine receptor; H3; antibody; histamine receptor protein;  
KW histamine; extracellular domain; extracellular loop; immunosuppressive;  
KW transmembrane domain; anti-allergic; antinflammatory; allergic reaction;  
KW anaphylactic shock; detection.

XX OS Homo sapiens.

XX PN DE10120816-A1.

XX PD 07-NOV-2002.

XX PF 27-APR-2001; 2001DE-01020816.

XX PR 27-APR-2001; 2001DE-01020816.

XX PA (SCHA/) SCHAEFER U.

XX PI Schaefer U;

DR WPI; 2003-168704/17.  
XX  
PT New antibody specific for histamine receptor protein, useful for treating  
PT or preventing e.g. allergy or inflammation, also antigens for its  
PT preparation.  
XX  
XX Claim 2; Fig 2C; 14pp; German.  
XX  
XX This invention describes a novel antibody that is specific for a  
CC histamine receptor protein (HRP), especially human, and is able to  
CC inhibit binding of histamine to HRP. The antibody is produced by  
CC immunisation with an antigenic polypeptide that comprises (i) an  
CC extracellular domain (ECD) having a sequence from the first extracellular  
CC loop (ECL) of HRP and optionally a transmembrane domain (TMD) having a  
CC sequence from the N-terminus of the third transmembrane region (TMR) of  
CC HRP, (ii) ECD having a sequence from the second ECL and optionally a TMD  
CC having a sequence from the C-terminus of the fourth TMR or (iii) an ECD  
CC having a sequence from the second ECL and optionally a TMD having a  
CC sequence from the N-terminus of the 5th TMR. The products of the  
CC invention have anti-allergic, anti-inflammatory and immunosuppressive  
CC activity. The antibodies are useful for (a) treating or preventing  
CC allergic reactions; chronic and/or acute inflammation and/or anaphylactic  
CC shock, in humans or animals and (b) diagnostic detection of HRP,  
CC especially in immunoassays. This sequence represents the human histamine  
CC receptor H3, described in the disclosure of the invention  
XX  
XX Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 6; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.1e-181;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVGLNALVMAFV 60  
DB 1 MERAPPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVGLNALVMAFV 60  
QY 61 ADSSLRQTQNNPFLNLAISDFLVGAFICPLYPYVYLTGRWTGRLGCKLWLVVDYLLCTS 120  
DB 61 ADSSLRQTQNNPFLNLAISDFLVGAFICPLYPYVYLTGRWTGRLGCKLWLVVDYLLCTS 120  
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILSWEYLSGG 180  
DB 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
QY 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300  
DB 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300  
QY 361 AVISIFGLCWAPYTLMLIIRAACHGCVDPDYYWYETSWLLWANSVNPVLPCHHSFR 420  
DB 361 AVISIFGLCWAPYTLMLIIRAACHGCVDPDYYWYETSWLLWANSVNPVLPCHHSFR 420  
QY 421 RAFTKLLCPQKLIKIPHSLSHCWK 445  
DB 421 RAFTKLLCPQKLIKIPHSLSHCWK 445

RESULT 7  
ABP59931  
ID ABP59931 standard; protein; 445 AA.  
XX  
AC ABP59931;  
XX  
DT 28-AUG-2003 (first entry)

DE Human histamine H3 receptor.  
XX  
KW Human; histamine H3 receptor; receptor modulator; agonist; nootropic;  
KW neuroprotective; cerebroprotective; cardiant; antiasthmatic;  
KW immunomodulator; gastrointestinal; antiallergic; antidiabetic;  
KW antiinflammatory; hypotensive; antiarrhythmic.  
XX  
OS Homo sapiens.  
XX  
XX WO20030404059-A1.  
XX  
XX 30-MAY-2003.  
XX  
XX 15-NOV-2001; 2001WO-US045313.  
XX  
XX 15-NOV-2001; 2001WO-US045313.  
XX  
XX (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
XX Lovenberg T;  
XX  
XX WPI; 2003-457595/43.  
XX  
XX N-PSDB; ACC59395.  
XX  
XX Identifying agonists of recombinant human histamine H3 receptor protein  
PT activity, useful for diagnosing and treating H3 receptor-related  
PT disorders, such as nervous system disorders, asthma, allergy,  
PT hypertension and diabetes.  
XX  
XX Example 1; Fig 3; 55pp; English.  
XX  
XX The present invention relates to a method of identifying compounds that  
CC are agonists of recombinant human histamine H3 receptor protein activity,  
CC comprising combining a compound suspected of being an antagonist of human  
CC histamine H3 receptor protein activity with recombinant human histamine  
CC H3 receptor protein, and measuring an agonistic effect of the compound on  
CC the recombinant human histamine H3 receptor protein. The methods and  
CC compositions of the present invention are useful for diagnosing and  
CC treating human histamine H3 receptor-related disorders, such as central  
CC and peripheral nervous system disorders (depression, anxiety, psychoses,  
CC Parkinson's disease, Alzheimer's disease, dementia and tardive  
CC dyskinesia), asthma, allergy, diabetes mellitus, inflammation, immune,  
CC cardiovascular (hypertension, and arrhythmia) and gastrointestinal  
CC disorders. The present sequence is the human histamine H3 receptor  
XX  
XX Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 6; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.1e-181;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVGLNALVMAFV 60  
DB 1 MERAPPDGLNAGSAGALAGDAAAAGGARGFSAATVLAALMALLIVATVGLNALVMAFV 60  
QY 61 ADSSLRQTQNNPFLNLAISDFLVGAFICPLYPYVYLTGRWTGRLGCKLWLVVDYLLCTS 120  
DB 61 ADSSLRQTQNNPFLNLAISDFLVGAFICPLYPYVYLTGRWTGRLGCKLWLVVDYLLCTS 120  
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILSWEYLSGG 180  
DB 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLYGPAILSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
QY 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300  
DB 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300  
QY 301 ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360



Db 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360  
 QY 361 AVIVSIFGLCWAPYTLMIIRACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420  
 Db 361 AVIVSIFGLCWAPYTLMIIRACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420  
 QY 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445  
 Db 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445

RESULT 8  
 ID AAO29527  
 XX AAO29527 standard; protein; 445 AA.  
 AC AAO29527;  
 DT 27-AUG-2003 (first entry)  
 XX  
 DE Human wild-type H3 receptor (H3a) protein.  
 XX  
 KW Human; H3 histamine receptor; central nervous system; depression; ulcer;  
 KW Tourette's syndrome; sexual dysfunction; drug addiction; cardiovascular;  
 KW anxiety; Parkinson's disease; Alzheimer's disease; obesity; arrhythmia;  
 KW constipation; gastrointestinal disorder; inflammation; cerebrovascular;  
 KW diabetes; hypertension; stress; allergy; prostate dysfunction; asthma;  
 KW gene therapy; receptor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003042359-A2.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 04-NOV-2002; 2002WO-US035375.  
 XX  
 PR 13-NOV-2001; 2001US-0333094P.  
 XX  
 PA (MERI ) MERCK & CO INC.  
 XX  
 PI Gallagher M, Yates SL;  
 XX  
 DR WPI; 2003-441792/41.  
 DR N-PSDB; AAL59976.  
 XX  
 PT New polynucleotide encoding a human H3 histamine receptor polypeptide,  
 PT useful for diagnosing or treating disorders associated with or modulated  
 PT by H3 histamine receptor, e.g. depression, anxiety, obesity, hypertension  
 PT or diabetes.  
 XX  
 PS Example; Page 50-51; 92pp; English.  
 XX  
 CC The invention relates to splice variants of human H3 histamine receptor  
 CC polypeptide and their corresponding polynucleotide sequences. The  
 CC invention is useful in diagnosing or treating diseases or disorders  
 CC associated with or modulated by the H3 histamine receptor, such as  
 CC central nervous system disorders (e.g. depression, anxiety, psychoses,  
 CC Parkinson's disease or Alzheimer's disease), obesity, hypertension,  
 CC Tourette's syndrome, sexual dysfunction, gastrointestinal disorders (e.g.  
 CC constipation), drug addiction, cardiovascular or cerebrovascular  
 CC disorders (e.g. arrhythmia), diabetes, stress, ulcers, asthma, allergy,  
 CC inflammation and prostate dysfunction. It is also used in gene therapy.  
 CC The polypeptide is useful for identifying agonists, antagonists or  
 CC inverse agonists of histamine action at the H3 receptor. The present  
 CC sequence is human wild-type H3 receptor protein  
 XX  
 SQ Sequence 445 AA;

Query Match 100.0%; Score 2361; DB 7; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-181;  
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGPLNAGLADGAAAAGGARGFSAANTAVLAALMALLIVATVGLNALVWLAFV 60

Db 1 MERAPPDGPLNAGLADGAAAAGGARGFSAANTAVLAALMALLIVATVGLNALVWLAFV 60  
 QY 61 ADSSLRTQNNFLLNLAISDFLVGAFCIPLVYPVYLTORWTFGRGLCKLWLVDYLLCTS 120  
 Db 61 ADSSLRTQNNFLLNLAISDFLVGAFCIPLVYPVYLTORWTFGRGLCKLWLVDYLLCTS 120  
 QY 121 SAFNIVLISYDRFSLVTRAVSYRAQGGDTRRAVRKMLLVWLAFLLYGPAILSWLYLGG 180  
 Db 121 SAFNIVLISYDRFSLVTRAVSYRAQGGDTRRAVRKMLLVWLAFLLYGPAILSWLYLGG 180  
 QY 181 SSIPEGHCHYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNITQRTLRLLDGARAA 240  
 Db 181 SSIPEGHCHYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNITQRTLRLLDGARAA 240  
 QY 241 GPEPPPEAQPSPPPPPGCGWQKQHGGEAMPLHRYGVGEAAVAGAEATLGGGGGGG 300  
 Db 241 GPEPPPEAQPSPPPPPGCGWQKQHGGEAMPLHRYGVGEAAVAGAEATLGGGGGGG 300  
 QY 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360  
 Db 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360  
 QY 361 AVIVSIFGLCWAPYTLMIIRACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420  
 Db 361 AVIVSIFGLCWAPYTLMIIRACHGHCVPDYWYETSFLLWANSVAVNPVLYPLCHHSFR 420  
 QY 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445  
 Db 421 RAFTKLLCPQKLIKIPHSSLEHCWK 445

RESULT 9  
 ID ADD22854  
 XX ADD22854 standard; protein; 445 AA.  
 AC ADD22854;  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human histamine H3 receptor.  
 XX  
 KW Human; Histamine H3 receptor; GPCR; G protein-coupled receptor; receptor;  
 KW immunogen; depression; anxiety; schizophrenia; Parkinson's disease;  
 KW obesity; hypertension; Tourette's syndrome; sexual dysfunction;  
 KW drug addiction; drug abuse; cognitive disorder; Alzheimer's disease;  
 KW obsessive-compulsive behaviour; panic attack; pain; eating disorder;  
 KW anorexia; cardiovascular disorder; cerebrovascular disorder; diabetes;  
 KW constipation; arrhythmia; ulcer; asthma; allergy; inflammation;  
 KW prostate dysfunction.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US6437100-B1.  
 XX  
 PD 20-AUG-2002.  
 XX  
 PF 21-AUG-2000; 2000US-00642514.  
 XX  
 PR 07-OCT-1998; 98US-00167354.  
 XX  
 PA (ORTH ) ORTHO PHARM CORP.  
 XX  
 PI Lovenberg TW, Erlander M, Huvar A, Pyati J;  
 XX  
 DR WPI; 2003-810293/76.  
 DR N-PSDB; ADD22860, ADD22861.  
 XX  
 PT New antibody against human histamine H3 receptor, preferably with  
 PT receptor antagonist activity, useful for diagnostic purposes and for  
 PT treating diseases such as depression, Parkinson's disease, obesity or  
 PT hypertension.

PS	Claim 1; SEQ ID NO 7; 25pp; English.	XX	05-AUG-2004.	XX
CC	The invention relates to a monospecific antibody immunologically reactive	PD		
CC	with a protein appearing as ADD22854, where the protein functions as a	XX		
CC	human histamine H3 receptor. The antibody blocks intracellular signaling	PF	14-JAN-2004; 2004WO-US000750.	XX
CC	activity of the human histamine H3 receptor in response to ligand	PR	15-JAN-2003; 2003US-0440318P.	
CC	binding. The antibody is useful for detecting and quantifying expression	PR	04-FEB-2003; 2003US-0444783P.	
CC	of human histamine H3 receptors, which may be useful for diagnostic,	PR	27-MAR-2003; 2003US-0457901P.	
CC	epidemiological or forensic purposes. The antibody is potentially useful	PR	08-MAY-2003; 2003US-0468775P.	
CC	in treating diseases such as depression, anxiety, schizophrenia,	PR	19-MAY-2003; 2003US-0471614P.	
CC	Parkinson's disease, obesity, hypertension, Tourette's syndrome, sexual	PR	16-JUN-2003; 2003US-0478742P.	
CC	dysfunction, drug addiction or drug abuse, cognitive disorders, sexual	PR	18-JUL-2003; 2003US-0488529P.	
CC	Alzheimer's disease, obsessive-compulsive behaviour, panic attacks, pain,	PR	30-JUL-2003; 2003US-0491156P.	
CC	eating disorders and anorexia, cardiovascular and cerebrovascular	PR	02-SEP-2003; 2003US-0499594P.	
CC	disorders, diabetes, constipation, arthritia, ulcers, asthma, allergy,	PR	26-SEP-2003; 2003US-0506332P.	
CC	inflammation, or prostate dysfunction. The present sequence represents	XX	(MILL-) MILLENNIUM PHARM INC.	
XX	the histamine H3 receptor.	PA		
SQ	Sequence 445 AA;	XX	Karicheti V, Silos-Santiago I, Eliasof SD;	
	Query Match 100.0%; Score 2361; DB 7; Length 445;	XX	WPI; 2004-562167/54.	
	Best Local Similarity 100.0%; Pred. No. 3.1e-181;	DR	N-PSDB; ADQ89179.	
	Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX		
QY	1 MERAPDGPINASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMAFV 60	PT	Use of polypeptides related to urological disorders, e.g. 44390, 54181,	
DB	1 MERAPDGPINASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVLGNALVMAFV 60	PT	211 or for identifying a compound capable of treating a urological	
QY	61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120	PT	disorder or identifying and treating a subject having a urological	
DB	61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120	XX	disorder.	
QY	121 SAFNVLISYDFLSVTRAVSYRAQQDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180	PS	Claim 1; SEQ ID NO 132; 542pp; English.	
DB	121 SAFNVLISYDFLSVTRAVSYRAQQDTRRAVRKMLLVWVLAFLYGPAILLSWEYLSGG 180	XX		
QY	181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240	CC	The present invention describes the use of polypeptides related to	
DB	181 SSIPGHCYAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240	CC	urological disorders for identifying a compound capable of treating a	
QY	241 GPEPPEAQSPPPPPGCGWKQKGHEAMPVLRHYGVGEAAVGAAGEATLGGGGGGSV 300	CC	urological disorder, identifying a subject having a urological disorder,	
DB	241 GPEPPEAQSPPPPPGCGWKQKGHEAMPVLRHYGVGEAAVGAAGEATLGGGGGGSV 300	CC	or treating a subject having a urological disorder. Also described: (1) a	
QY	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFQRPFLSRDRKVKSL 360	CC	method for identifying a compound capable of treating a urological	
DB	301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMVSQSFQRPFLSRDRKVKSL 360	CC	disorder; (2) a method for identifying a subject having a urological	
QY	361 AVISIFGLCWAPYTLMLTIRAAACHGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFR 420	CC	disorder; and (3) a method for treating a subject having a urological	
DB	361 AVISIFGLCWAPYTLMLTIRAAACHGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFR 420	CC	disorder. The compound has uropathic and cytostatic activities. The	
QY	421 RAFTKLLCQKLIKIOPHSSLEHCWK 445	CC	polypeptides related to urological disorders are useful for identifying a	
DB	421 RAFTKLLCQKLIKIOPHSSLEHCWK 445	CC	compound capable of treating a urological disorder, identifying a subject	
	RESULT 10	CC	having a urological disorder, or treating a subject having a urological	
ADQ89180	ADQ89180 standard; protein; 445 AA.	CC	disorder. Disorders include urinary incontinence and benign prostatic	
XX	ADQ89180;	CC	hyperplasia. The present sequence represents a human urological disorder	
XX	21-OCT-2004 (first entry)	CC	related protein, which is used in the exemplification of the present	
DE	Human urological disorder related protein 8203 SEQ.132.	XX	invention.	
KW	urological disorder; uropathic; cytostatic; urinary incontinence;	SQ	Sequence 445 AA;	
KW	benign prostatic hyperplasia; human.			
OS	Homo sapiens.			
XX	WO2004065576-A2.			

```
Db 301 ASPTSSSSSGTGRPRSLKSGSPASSASLEKRMKMWVSQFTQRLSRDRKVAKSL 360
QY 361 AVISIFGLCWAPYTLMIIRAACHGHCVPDYWYETSPWLLWANSVNPVLYPLCHHSFR 420
Db 361 AVISIFGLCWAPYTLMIIRAACHGHCVPDYWYETSPWLLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKPHSSLEHCWK 445
Db 421 RAFTKLLCPQKLIKPHSSLEHCWK 445

RESULT 11
ADR31458
ID ADR31458 standard; protein; 445 AA.
AC ADR31458;
DT 04-NOV-2004 (first entry)
DE Human histamine H3 receptor protein.
KW Human; Parkinson's disease; obesity; Alzheimer's disease; pain; stress;
KW ulcer; constipation; non-insulin dependent diabetes mellitus;
KW histamine H3 receptor; receptor.
XX
OS Homo sapiens.
XX
XX US2004156845-A1.
XX
XX 12-AUG-2004.
XX
XX 02-DEC-2003; 2003US-00727021.
XX
XX 07-OCT-1998; 98US-00167354.
XX
XX 21-AUG-2000; 2000US-00642852.
XX
XX (LOVE/) LOVENBERG T W.
XX (ERLA/) ERLANDER M.
XX (HUA/) HUVAR A.
XX (PYAT/) PYATI J.
XX
XX Lovenberg TW, Erlander M, Huvar A, Pyati J;
XX
XX WPI; 2004-592726/57.
XX
XX N-PSDB; ADR31456, ADR31457.
XX
XX Novel isolated and purified human histamine H3 receptor protein useful
XX for identifying modulators utilized for treating Parkinson's disease,
XX obesity, Alzheimer's disease, pain, stress or ulcers.
XX
XX Claim 11; SEQ ID NO 7; 26pp; English.
XX
XX The present invention provides a human histamine H3 receptor protein and
XX nucleic acid encoding such protein. The invention is useful for
XX identifying compounds that modulate the activity of human histamine H3
XX receptor. The invention is useful for treating a condition that is
XX mediated by a human histamine H3 receptor in a patient and for treating
XX Parkinson's disease, obesity, Alzheimer's disease, pain, stress, ulcers,
XX constipation and non-insulin dependent diabetes mellitus. The present
XX sequence is a human histamine H3 receptor protein.
XX
XX Sequence 445 AA;
XX
XX Query Match 100.0%; Score 2361; DB 8; Length 445;
XX Best Local Similarity 100.0%; Pred. No. 3.1e-181;
XX Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGPINAGLAGDAAAAGARGPSAAWTAVALMALMALLIVATVIGNALVMLAPV 60
Db 1 MERAPPDGPINAGLAGDAAAAGARGPSAAWTAVALMALMALLIVATVIGNALVMLAPV 60
QY 61 ADSSLRTQNNFFLLNLAISDFLVGAFCLPLYPVYLGTGRWTFGRGLCKLWLVVDYLCT 120
```

```
Db 61 ADSSLRTQNNFFLLNLAISDFLVGAFCLPLYPVYLGTGRWTFGRGLCKLWLVVDYLCT 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAARVKKMLLVWVLAFLLYGPAILSWEYLSGG 180
Db 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAARVKKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFPFLNLSIYLNQRTLRDLGAREAA 240
Db 181 SSIPEGHCYAEFFYNWYFLITASTLEFFTPFLSVTFPFLNLSIYLNQRTLRDLGAREAA 240
QY 241 GPEPPPEAQPSPPPPPGCGWQKQHGCEAMPLHRYGVGEAAVGAEGEATLGGGGGGGSV 300
Db 241 GPEPPPEAQPSPPPPPGCGWQKQHGCEAMPLHRYGVGEAAVGAEGEATLGGGGGGGSV 300
QY 301 ASPTSSSSSGTGRPRSLKSGSPASSASLEKRMKMWVSQFTQRLSRDRKVAKSL 360
Db 301 ASPTSSSSSGTGRPRSLKSGSPASSASLEKRMKMWVSQFTQRLSRDRKVAKSL 360
QY 361 AVISIFGLCWAPYTLMIIRAACHGHCVPDYWYETSPWLLWANSVNPVLYPLCHHSFR 420
Db 361 AVISIFGLCWAPYTLMIIRAACHGHCVPDYWYETSPWLLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIKPHSSLEHCWK 445
Db 421 RAFTKLLCPQKLIKPHSSLEHCWK 445

RESULT 12
AAW92975
ID AAW92975 standard; protein; 445 AA.
XX
XX AAW92975;
XX
XX 14-MAY-1999 (first entry)
XX
XX Human mACHR-6 protein.
XX
XX mACHR-6; muscarinic acetylcholine receptor 6; disorder; secretion;
XX acetylcholine responsive cell; phosphatidylinositol turn-over;
XX smooth muscle cell contraction; nervous system disorder; glandular;
XX schizo-effective disorder; affective disorder; sleep disorder;
XX movement disorder; eating disorder; drinking disorder; human.
XX
XX Homo sapiens.
XX
XX US5882893-A.
XX
XX 16-MAR-1999.
XX
XX 04-DEC-1997; 97US-00985090.
XX
XX 04-DEC-1997; 97US-00985090.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Goodearl AD;
XX
XX WPI; 1999-214063/18.
XX
XX N-PSDB; AAX02885, AAX02886.
XX
XX Nucleic acids encoding muscarinic acetylcholine receptor 6 - useful for
XX modulating the effects of acetylcholine on acetylcholine responsive
XX cells.
XX
XX Claim 1a; Fig 1A-D; 59pp; English.
XX
XX This invention describes the isolation of a novel human muscarinic
XX acetylcholine receptor 6 (mACHR-6), capable of modulating the effects of
XX acetylcholine on acetylcholine responsive cells. mACHR-6 cDNAs and
XX polypeptides may be used to detect naturally occurring mutations of the
XX mACHR-6 gene and determine if a subject with the mutated gene is at risk
XX of (or is predisposed to have) a mACHR-6 related disorder, modulate cell
```

CC activity mediated by mACHR-6 (e.g. biological processes mediated by  
CC phosphatidylinositol turn-over and signalling), secretion of a molecule  
CC (e.g. a neurotransmitter or a glandular enzyme), or contraction of a  
CC smooth muscle cell, treat disorders mediated by abnormal mACHR-6 activity  
CC e.g nervous system disorders (e.g. amnesia, apraxia, agnosia, amnesic  
CC dysnomia, amnesic spatial disorientation, Klüver-Bucy syndrome,  
CC Alzheimer's related memory loss and learning disability, visual  
CC hallucinations, perceptual disturbances, and Lewy body dementia  
CC associated delirium), schizo-effective disorders (e.g schizophrenia with  
CC mood swings, and depressive illness), affective disorders, sleep  
CC disorders (e.g. REM sleep abnormalities, paradoxical sleep abnormalities,  
CC sleep-wakefulness, and body temperature or respiratory depression  
CC abnormalities during sleep), pain generating mechanism disorders (e.g.  
CC related to irritable bowel syndrome (IBS), or chest pain), movement  
CC disorders (e.g. related to Parkinson's disease), eating disorders (e.g.  
CC insulin hypersecretion related obesity), drinking disorders (e.g.  
CC diabetic polydipsia), smooth muscle related disorders (e.g. IBS,  
CC diverticular disease, urinary incontinence, oesophageal achalasia, and  
CC chronic obstructive airways disease), cardiac disorders (e.g pathologic  
CC bradycardia or tachycardia, arrhythmia, flutter and fibrillation), and  
CC glandular disorders (e.g. xerostomia and diabetes mellitus)  
XX  
SQ Sequence 445 AA;

Query Match 99.8%; Score 2357; DB 2; Length 445;  
Best Local Similarity 99.8%; Pred. No. 6.5e-181;  
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPDGLNAGALAGAAAGARGSAWTAVALAALMALLIVATVGLNALVWLAFV 60  
DB 1 MERAPDGLNAGALAGAAAGARGSAWTAVALAALMALLIVATVGLNALVWLAFV 60

QY 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRTGRCGLKWLVDVLLCTS 120  
DB 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRTGRCGLKWLVDVLLCTS 120

QY 121 SAFNVLISYDFLSVTRAVSRAQGDTRRAVRKMLLVWLAFLLYGPAILLSWEYLSGG 180  
DB 121 SAFNVLISYDFLSVTRAVSRAQGDTRRAVRKMLLVWLAFLLYGPAILLSWEYLSGG 180

QY 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNNLSIYNTQRTRLDGAEEA 240  
DB 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNNLSIYNTQRTRLDGAEEA 240

QY 241 GPEPPEAQSPPPPGCGWKQKGHEAMPLHRYGVGEAAVCAAGEATLGGGGGGSV 300  
DB 241 GPEPPEAQSPPPPGCGWKQKGHEAMPLHRYGVGEAAVCAAGEATLGGGGGGSV 300

QY 301 ASPTSSSGSSRGTERPSLRKSKSPASSASLEKRMKMWVSQFTQRPRLSRDKVAKSL 360  
DB 301 ASPTSSSGSSRGTERPSLRKSKSPASSASLEKRMKMWVSQFTQRPRLSRDKVAKSL 360

QY 361 AVISIFGLCWAPYLLMIIRAACHGCVDPDYWYETSFLLWANSANVPVLPCHHSFR 420  
DB 361 AVISIFGLCWAPYLLMIIRAACHGCVDPDYWYETSFLLWANSANVPVLPCHHSFR 420

QY 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445  
DB 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445

RESULT 13  
AAV06322  
ID AAY06322 standard; protein; 445 AA.  
AC AAY06322;  
XX  
XX  
DT 06-SEP-1999 (first entry)  
XX  
DE Human G protein coupled receptor flh84g5.  
XX  
KW G protein coupled receptor; flh84g5; human; diagnosis; screening;  
KW therapy; antiparkinsonian; nootropic; neuroprotective; neuroleptic;

KW antidepressant; antiarrhythmic; antidiabetic; antiinflammatory;  
KW phosphatidylinositol.  
XX  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Domain 34..59  
FT Domain /note= "transmembrane domain"  
FT Domain 73..91  
FT Domain /note= "transmembrane domain"  
FT Domain 109..130  
FT Domain /note= "transmembrane domain"  
FT Domain 152..174  
FT Domain /note= "transmembrane domain"  
FT Domain 197..219  
FT Domain /note= "transmembrane domain"  
FT Domain 360..380  
FT Domain /note= "transmembrane domain"  
FT Domain 396..416  
FT Domain /note= "transmembrane domain"  
XX  
PN W09928470-A1.  
XX  
XX  
PD 10-JUN-1999.  
XX  
XX 04-DEC-1999; 98WO-US025832.  
XX  
PR 04-DEC-1997; 97US-00985090.  
PR 17-MAR-1998; 98US-00042780.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Goodearl ADJ, Glucksmann MA, Xie M, Distefano P;  
XX  
XX WPI: 1999-394858/33.  
DR N-PSDB; AAX59167.  
XX  
XX New nucleic acid encoding an isolated G-protein coupled receptor useful  
XX for treating nervous system related disorders.  
XX  
XX Claim 8a; Fig 1; 14Opp; English.  
XX  
XX The present sequence represents a novel human G protein coupled receptor,  
XX termed flh84g5, as deduced from a human cerebellum cDNA clone (see  
XX AAX59167). The invention provides human, rat and mouse flh84g5  
XX polynucleotides (including polynucleotides encoding the transmembrane  
XX regions of flh84g5 and antisense nucleic acid molecules), expression  
XX vectors, host cells, transgenic animals, flh84g5 polypeptides and  
XX antibodies, and a method of modulating phosphatidylinositol metabolism.  
XX The flh84g5 polypeptides can (i) interact with a flh84g5 ligand, such as  
XX acetylcholine or carnitine, (ii) interact with a G protein or another  
XX protein which naturally binds to flh84g5, (iii) modulate the activity of  
XX an ion channel (e.g. a calcium activated chloride channel or a potassium  
XX or calcium channel), (iv) modulate cytosolic ion, e.g. calcium  
XX concentration, (v) modulate the release of a neurotransmitter, e.g.  
XX acetylcholine or carnitine from a neuron, (vi) modulate a flh84g5 ligand  
XX response in a responsive cell, (vii) signal ligand binding via  
XX phosphatidylinositol turnover, and (viii) modulate phospholipase C  
XX activity. The products can be used to treat: disorders mediated by  
XX abnormal flh84g5 polypeptide activity such as nervous system related  
XX disorders, e.g. amnesia, apraxia, agnosia, amnesic dysnomia, amnesic  
XX spatial disorientation, Klüver-Bucy syndrome, Alzheimer's related memory  
XX loss and learning disability; disorders affecting consciousness such as  
XX visual hallucinations, perceptual disturbances or delirium associated  
XX with Lewy body dementia, schitzo-effective disorders, schizophrenia with  
XX mood swings, depressive illness (primary and secondary); affective  
XX disorders such as REM sleep abnormalities in patients suffering from e.g.  
XX depression, paradoxical sleep abnormalities, sleep-wakefulness, and body  
XX temperature or respiratory depression abnormalities during sleep;  
XX disorders affecting pain generation mechanisms e.g. pain related to  
XX irritable bowel syndrome or chest pain; movement disorders e.g.  
XX Parkinson's disease related movement disorders; eating disorders e.g.  
XX insulin hypersecretion related obesity or drinking disorders, e.g.

```
CC diabetic polydipsia; smooth muscle related disorders, e.g. irritable
CC bowel syndrome, diverticular disease, urinary incontinence, oesophageal
CC achalasia or chronic obstructive airways disease; cardiac muscle
CC disorders, e.g. pathologic bradycardia or tachycardia, arrhythmia,
CC flutter or fibrillation; and gland related disorder such as xerostomia or
CC diabetes mellitus. The products can also be used for detection, diagnosis
XX and drug screening
XX
SQ Sequence 445 AA;

Query Match          99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 6.5e-181;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGPLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
Db 1 MERAPPDGPLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
Db 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNQTRTRLDGAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNQTRTRLDGAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWKQGHGEMPLHRYGVGEAAVGAEGEATLGGGGGGGSV 300
Db 241 GPEPPEAQSPPPPPGCGWKQGHGEMPLHRYGVGEAAVGAEGEATLGGGGGGGSV 300
QY 301 ASPTSSSSSSSGRTSRPSLRKSGKSPASASSLEKRMKMVSQSFQRFSLGRDRKVAKSL 360
Db 301 ASPTSSSSSSSGRTSRPSLRKSGKSPASASSLEKRMKMVSQSFQRFSLGRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMIIRACHGCVDPDYWYETSPWLLWANSVNPVLYPLCHHSFR 420
Db 361 AVIVSIFGLCWAPYTLMIIRACHGCVDPDYWYETSPWLLWANSVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCPQKLIQPHSSLEHCWK 445
Db 421 RAFTKLLCPQKLIQPHSSLEHCWK 445

RESULT 14
AAG67830
ID AAG67830 standard; protein; 445 AA.
XX
AC AAG67830;
XX
DT 20-MAR-2003 (revised)
DT 01-NOV-2001 (first entry)
XX
DE Human muscarinic acetylcholine receptor protein SEQ ID NO:2.
XX
KW Human; muscarinic acetylcholine receptor 6; mAChR-6; detection;
KW antiparkinsonian; nootropic; neuroprotective; neuroleptic; antidiabetic;
KW antidepressant; antiarrhythmic; antiinflammatory; carnitine; pain;
KW G-protein coupled receptor; nervous system related disorder; xerostomia;
KW disorders affecting consciousness; affective disorder; movement disorder;
KW irritable bowel syndrome; drinking disorder; gland related disorder;
KW smooth muscle related disorder; cardiac muscle disorder; eating disorder;
KW diabetes mellitus; diagnosis; drug screening.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 34..59
FT /label= transmembrane_domain
FT 73..91
FT Domain
```

```
FT Domain /label= transmembrane_domain
FT 109..130
FT /label= transmembrane_domain
FT 152..174
FT /label= transmembrane_domain
FT 197..219
FT /label= transmembrane_domain
FT 360..380
FT /label= transmembrane_domain
FT 396..416
FT /label= transmembrane_domain
PN US6093545-A.
XX
PD 25-JUL-2000.
XX
PF 02-OCT-1998; 98US-00165543.
PR 04-DEC-1997; 97US-00985090.
PR 17-MAR-1998; 98US-00042780.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Glucksmann MA, Goodearl ADJ;
XX
DR WPI; 1999-394858/33.
DR N-PSDB; AAH44572, AAH44573.
XX
PT New nucleic acid encoding an isolated G-protein coupled receptor useful
PT for treating nervous system related disorders.
XX
PS Claim 1; Fig 1; 64pp; English.
XX
CC The present sequence represents human muscarinic acetylcholine receptor 6
CC (mAChR-6), which is a member of the G family of proteins. mAChR-6 has
CC antiparkinsonian, nootropic, neuroprotective, neuroleptic, antidiabetic
CC antidepressant, antiarrhythmic and antiinflammatory activities. The mAChR
CC -6 protein, is capable of modulating the effects of a G-protein coupled
CC receptor (GPCR) ligand such as acetylcholine or an acetylcholine like
CC molecule such as carnitine, e.g. by modulating phospholipase C
CC signalling/activity. Products from the present invention can be used for
CC treating disorders mediated by abnormal mAChR-6 protein activity such as
CC nervous system related disorders, disorders affecting consciousness,
CC affective disorders such as REM sleep abnormalities, disorders affecting
CC pain generation mechanisms such as pain related to irritable bowel
CC syndrome or chest pain, movement disorders, eating disorders, drinking
CC disorders, smooth muscle related disorders, cardiac muscle disorders, and
CC gland related disorders such as xerostomia or diabetes mellitus. The
CC products can also be used for detection, diagnosis and drug screening.
CC (Updated on 20-MAR-2003 to correct DR field.)
XX
SQ Sequence 445 AA;

Query Match          99.8%; Score 2357; DB 2; Length 445;
Best Local Similarity 99.8%; Pred. No. 6.5e-181;
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERAPPDGPLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
Db 1 MERAPPDGPLNAGSALAGDAAAAGARGFSAWTAVALAALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNFFLLNLATSDFLVGAFCTPLVYPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
Db 121 SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNQTRTRLDGAREAA 240
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNNLSIYLNQTRTRLDGAREAA 240
```

241	Qy	GPPEPPEAQSPPPPPGCGWQKHGHEAMP	PHRYGVGEAAVGAAGEATLGGGGGGGSV	300
241	Db	GPPEPPEAQSPPPPPGCGWQKHGHEAMP	PHRYGVGEAAVGAAGEATLGGGGGGGSV	300
301	Qy	ASPTSSSSSGSGTERPESLKRGGKPSASSAS	LEKRMKMWVSQSFTQRFRLSRDRKVAKSL	360
301	Db	ASPTSSSSSGSGTERPESLKRGGKPSASSAS	LEKRMKMWVSQSFTQRFRLSRDRKVAKSL	360
361	Qy	AVIVSIFGLCWAPYTLMIIRAAACHGHG	CPDPYWTETSFLLWANSANVPVLPCHHSFR	420
361	Db	AVIVSIFGLCWAPYTLMIIRAAACHGHG	CPDPYWTETSFLLWANSANVPVLPCHHSFR	420
421	Qy	RAFTKLLCPQKLIKIPHSSLSHCWK	445	
421	Db	RAFTKLLCPQKLIKIPHSSLSHCWK	445	

**RESULT 15**

ABR433667  
ID ABR433667 standard; protein; 445 AA.

DT 24-JUL-2003 (first entry)

Human histamine H3 receptor protein.

Histamine H3 receptor; aminoazetidine; pyrrolidine; piperidine; anorectic; anabolic; antidiabetic; antiallergic; antiinflammatory; antitumor; nootropic; neuroprotective; tranquilliser; antiemetic; antiasthmatic; antilipaeamic; cardiac; osteopathic; antiarthritic; auditory; cytostatic; overweight; obesity; eating disorder; bulimia binge eating; impaired glucose tolerance; type 2 diabetes; ulcer; allergic rhinitis; anorexia; Alzheimer's disease; narcolepsy; attention deficit disorder; dementia; motion sickness; vertigo; irritable bowel syndrome; gall bladder disease; cancer; narcolepsy; attention deficit disorder; airway disorder; asthma; dyslipidaemia; coronary heart disease; osteoarthritis.

OS Homo sapiens.

XX PN WO2003024928-A2.

27-MAR-2003.

11-SEP-2002: 2002WO-DK000593.

14-SEP-2001: 2001DK-000001344.

FR 14-SEP-2001; 2001DK-00001344;  
PR 16-MAY-2002; 2002DK-00000750.

PA (NOVO ) NOVO NORDISK AS.

PA (BOEH ) BOEHRINGER INGELHEIM INT GMBH.

PI Doerwald FZ, Hohlweg R;

WPI: 2003-363111/34.

Use of new and known aminoazetidine, pyrrolidine and piperidine derivatives for treating diseases related to histamine H3 receptor e.g. obesity, Alzheimer's disease and type 2 diabetes.

PS Example; Page 38; 54pp; English.

The present invention describes aminoazetidine, pyrrolidine and piperidine derivatives (I), which are used for the treatment of disorders and diseases related to the histamine H3 receptor. (I) have anorectic, anabolic, antidiabetic, anti-allergic, antiinflammatory, antiulcer, neurotropic, neuroprotective, tranquilliser, antiemetic, antiaesthetic, antihypaemic, cardiant, osteopathic, antiarthritic, auditory and cyostatic activities. (I) can be used for treating and/or preventing diseases and disorders related to H3 histamine receptor e.g. overweight or obesity, eating disorders (e.g. bulimia and binge eating), impaired glucose tolerance, type 2 diabetes, allergic rhinitis, ulcer, anorexia,

Alzheimer's disease, narcolepsy and attention deficit disorder, for the delaying or preventing the progression from non-insulin requiring type 2 diabetes to insulin requiring type 2 diabetes, for reducing weight and suppressing appetite or satiety induction. (I) can also be used for treating dementia, motion sickness, vertigo, irritable bowel syndrome, gall bladder disease, cancer of breast, prostate and colon, narcolepsy, attention deficit disorder, airway disorders (e.g. asthma), dyslipidaemia, coronary heart disease and osteoarthritis. (I) have high and selective binding affinity to the histamine H3 receptor. The present sequence represents the human histamine H3 receptor protein, which is given in the exemplification of the present invention

Sequence 445 AA:

Query Match 99.8%: Score 2357: DB 6: Length 445:

Best Local Similarity 99.8%; Pred. No. 6.5e-181;

Best local similarity 55.6%, Rec: NO, 0.50 101,  
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QV 1 MERAPPDGPLNASGALAGDAAAAGGARGFSAAWTAVLALMALLIVATVLGNALVMLAFV 60

[illegible]

DD I MERN AFFDGE UNASSOATTHANESHTAGGARGTSAWIAV DGNAD VMETAFV 00

QY 61 ADSSLRTQNNFFLLNLAI SDFLVGAFCIPLYPYVLTGRWTFGRGLCKLWLVDYLLCTS 120

61 ADSSLRTONFFLLNLAISDFLVGAFCIPLVVPYVLTGRWTFGRGLCKLWLVPDYLLCTS 120

[illegible]

QY 121 SAFNIVLISIDRFLSVIRAVSIRAQQGDIRRAVRKMLLVWLAFLIYGPAILSWEYLSGS 180

db 121 SAFNIVLISYDRELSVTTRAVSYRAOOGDTRRAVRKMLLVVLAFLLYGPAILSWEYLSGG 180

181 SSIPEGHCHYAEFFYNWYFLITASTIEFFTPEI,SVTPFNI,STYI,NTORRTRI,RI,DGAREAA 240 QV

QY 181 SSIPEGHCAEFFFNWIFLTIASILEFFIPFFLSVIFFFNLSTIYLN1QRRIRLRDLGAREAA 240

DB 181 SSIPEGHCYAEFFYNWYFLTIASITLLEFFIIPFLSVIFFNLSTYLNIQRRIRLRDLGAREAA 240

241 GPEPPPEAQPSPPPPPGCGWCGWKGHGEAMPIHRYGVGEAAVGAEGEATI.GGGGGGGSV 300

241 GPEPPPEAOPSPPPPPCWCWCKHCFAMPIHPYCVCFRAAYCAFACFATCCCGCCGCSV 300

DB 241 GPEPPPEAQPSPPPPPPGCGCQKQGHGEAMPLHRYIGVGEAAVGAEGEATLGGGGGGSV 300

301 ASPTSSGSSSRGTERPSRLKRGSKPSAS  
QY

301 ASDTSSSSSSSCTETFPBPST-KPCGSKPSAS

Search completed: June 2, 2005. 20:39:18

search completed:  
Job time : 87 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 19:07:00 ; Search time 24 Seconds  
(without alignments)  
1784.019 Million cell updates/sec

Title: US-10-727-021-7  
Perfect score: 2361  
Sequence: 1 MERAPPDGLNASGALGDA.....LLCPQKLIKPHSSLEHCWK 445  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	724	30.7	390	JC7566	histamine H4 recep
2	592	25.1	460	I51837	muscarinic recepto
3	592	25.1	460	A29514	muscarinic acetyl
4	591.5	25.1	460	S09508	muscarinic acetyl
5	587.5	24.9	460	A24325	muscarinic acetyl
6	578	24.5	460	A31897	muscarinic acetyl
7	553.5	23.4	590	S47572	muscarinic acetyl
8	546.5	23.1	590	S01114	muscarinic acetyl
9	541	22.9	590	S10128	muscarinic acetyl
10	539	22.8	589	B29514	muscarinic acetyl
11	536	22.7	479	S10127	muscarinic acetyl
12	535	22.7	479	S33776	muscarinic acetyl
13	532.5	22.6	478	C29514	muscarinic acetyl
14	527.5	22.3	532	JT0530	muscarinic acetyl
15	525.5	22.3	466	JH0197	muscarinic acetyl
16	525.5	22.3	589	A29476	muscarinic acetyl
17	524.5	22.2	466	S10856	muscarinic acetyl
18	523.5	22.2	531	JT0531	muscarinic acetyl
19	517.5	21.9	466	A40972	muscarinic acetyl
20	517.5	21.9	466	S10126	muscarinic acetyl
21	512.5	21.7	466	A27386	muscarinic acetyl
22	511	21.6	639	A55019	muscarinic acetyl
23	505.5	21.4	450	A38316	muscarinic acetyl
24	504	21.3	490	A35546	muscarinic acetyl
25	498.5	21.1	601	JH0170	octopamine recepto
26	498.5	21.1	601	S12004	tyramine receptor
27	493.5	20.9	461	A31237	alpha-2C-adrenerg
28	489.5	20.7	432	I50829	alpha 2-adrenocept
29	485.5	20.6	450	I49481	alpha-2 adrenergic

30 485 20.5 455 2 S28221 alpha-2-C2 adrener  
31 484.5 20.5 450 2 A34169 alpha-2A-adrenerg  
32 480.5 20.4 450 2 B40392 alpha-2-adrenerg  
33 479 20.3 484 2 S48657 muscarinic acetyl  
34 478 20.2 448 2 I51883 alpha-2B-adrenerg  
35 478 20.2 458 2 I49480 alpha-2 adrenergic  
36 478 20.2 458 2 A40392 alpha-2-adrenerg  
37 473 20.0 450 2 A37223 alpha-2B-adrenerg  
38 472 20.0 458 2 A37869 alpha-2B-adrenerg  
39 469 19.9 453 2 A35642 alpha-2B-adrenerg  
40 468.5 19.8 450 2 JH0190 histamine H1 recep  
41 468 19.8 491 2 A41632 G protein-coupled  
42 467 19.8 476 2 JC5042 alpha 2C4 adrenoce  
43 466 19.7 458 2 A48392 G protein-coupled  
44 466 19.7 484 2 S58868 histamine H1 recep  
45 466 19.7 486 2 JC1415

RESULT 1  
JC7566  
histamine H4 receptor, HH4R - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: JC7566  
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A>Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A:Reference number: JC7566; MUID: 20568725; PMID:1118334  
A:Contents: Leukocyte  
A:Accession: JC7566  
A:Molecule type: mRNA  
A:Residues: 1-390 <NAK>  
A:Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370  
C:Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled  
C:Genetics:  
A:Gene: hh4r  
C:Keywords: G protein-coupled receptor; transmembrane protein

ALIGNMENTS

QY 432 LKIQP 436

Db 375 IKQP 379

## RESULT 2

151837

muscarinic receptor - rat

C:Species: Rattus sp. (rat)

C&gt;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 24-Nov-1999

C:Accession: I51837

R:Li, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roeske

Adv. Exp. Med. Biol. 287, 313-330, 1991

A&gt;Title: The molecular properties of the M1 muscarinic receptor and its regulation of cy

A:Reference number: I51837; MUID:92101806; PMID:1759615

A:Accession: I51837

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-460 &lt;RES&gt;

A:Cross-references: GB:S73971; NID:g241253; PIDN:AAB20705.1; PID:g241254

C:Genetics:

C:Gene: ml

C:Superfamily: vertebrate rhodopsin

Query Match 25.1%; Score 592; DB 2; Length 460;

Best Local Similarity 33.7%; Pred. No. 2.8e-34;

Matches 149; Conservative 66; Mismatches 149; Indels 78; Gaps 17;

QY 33 W-TAVLAALMALLIVATVLGNALVAFVADSSLRTONNFLLNLAISDFLVGAFCIPLY 91

Db 23 WQVAFIGITGLSLATVTGNLLVLSFKVNTLKTNNYFLLSLACADLIIGTFSMNLY 82

QY 92 VPYVLTGRWTFGRGLCKLWVDYLLCTSSAFNVLISYDRFLSVTRAVSRAOQDTRR 151

Db 83 TTYLLMGHWALGTACDLWLALDYVNASVNMNLLISFDYFVSTRPLSYRAKR-TPRR 141

QY 152 AVRKMLLVMVLAFLYGPAILSWEYLSGSSSIPEGHCAEFPYNNYFLITASTLFFTFPF 211

Db 142 AALMTGLAWLSFVLAFAILLFWQVLGERTVLAGQCIQFLSQPIIFGTAMAAFYLP- 200

QY 212 LSVTFNFIISYINIQRRTRLRLDGAEEA---GPEPP-----PEAQSPPPP 254

Db 201 --VTVM-CTLYWRIYRETNR---ARELAALQSGSETPGKGGSSSSSSSQPGAEGSPES 254

QY 255 PPG-CWGC-----WQKHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGGVA- 301

Db 255 PPGRCRCRCPRLQLQAYSWKEEBE-----DEGSMEISLTSEGEPP-----GSEVVI 302

QY 302 -----SPTSSSGSSSRGT-ERPRSLKR-----GSKPSASSASLEKMKMVSQSFT 345

Db 303 KMPWVDSEAQAFTKQPKSSPNTVKRPTKKGDRGKGQKPRKE-QLAKR----- 352

QY 346 QRFLSRDRKVAKSIAVIVSIFGLCWAPYTLMIIRAAACHGHCVPDYWYETSFLLWANS 405

Db 353 KTFSLVKEKKAARTLSAILLAFILTWTPYINIMVLVSTFCK-DCVPETLWELGYLWCYVNS 411

QY 406 AVNPVLYPLCHHSFRRAFTKLL 427

Db 412 TVNPMCYALCNKAFRDTFRLLL 433

## RESULT 3

A29514

muscarinic acetylcholine receptor M1 - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004

C:Accession: A94518; A94293; A37121; A29514

R:Bonner, T.I.

submitted to GenBank, July 1987

A:Reference number: A94518

A:Accession: A94518

A:Molecule type: mRNA

A:Residues: 1-460 &lt;BO1&gt;

A:Cross-references: UNIPROT:P08482

R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.

Science 237, 527-532, 1987

A&gt;Title: Identification of a family of muscarinic acetylcholine receptor genes.

A:Reference number: A94293; MUID:87263421; PMID:3037705

A:Accession: A94293

A:Molecule type: mRNA

A:Residues: 1-227;338-460 &lt;BO2&gt;

A:Experimental source: cerebral cortex

A&gt;Note: only a part of the protein translation is given; none of the nucleotide sequence

R:Kurténbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.

J. Biol. Chem. 265, 13702-13708, 1990

A&gt;Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invol

A:Reference number: A37121; MUID:90337982; PMID:2380182

A:Accession: A37121

A&gt;Status: preliminary

A:Molecule type: protein

A:Residues: 62-124 &lt;KUR&gt;

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:25-50/Domain: transmembrane #status predicted &lt;TM1&gt;

F:62-93/Domain: transmembrane #status predicted &lt;TM2&gt;

F:100-121/Domain: transmembrane #status predicted &lt;TM3&gt;

F:142-168/Domain: transmembrane #status predicted &lt;TM4&gt;

F:187-209/Domain: transmembrane #status predicted &lt;TM5&gt;

F:367-387/Domain: transmembrane #status predicted &lt;TM6&gt;

F:402-420/Domain: transmembrane #status predicted &lt;TM7&gt;

F:2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.1%; Score 592; DB 2; Length 460;

Best Local Similarity 33.7%; Pred. No. 2.8e-34;

Matches 149; Conservative 66; Mismatches 149; Indels 78; Gaps 17;

QY 33 W-TAVLAALMALLIVATVLGNALVAFVADSSLRTONNFLLNLAISDFLVGAFCIPLY 91

Db 23 WQVAFIGITGLSLATVTGNLLVLSFKVNTLKTNNYFLLSLACADLIIGTFSMNLY 82

QY 92 VPYVLTGRWTFGRGLCKLWVDYLLCTSSAFNVLISYDRFLSVTRAVSRAOQDTRR 151

Db 83 TTYLLMGHWALGTACDLWLALDYVNASVNMNLLISFDYFVSTRPLSYRAKR-TPRR 141

QY 152 AVRKMLLVMVLAFLYGPAILSWEYLSGSSSIPEGHCAEFPYNNYFLITASTLFFTFPF 211

Db 142 AALMTGLAWLSFVLAFAILLFWQVLGERTVLAGQCIQFLSQPIIFGTAMAAFYLP- 200

QY 212 LSVTFNFIISYINIQRRTRLRLDGAEEA---GPEPP-----PEAQSPPPP 254

Db 201 --VTVM-CTLYWRIYRETNR---ARELAALQSGSETPGKGGSSSSSSSQPGAEGSPES 254

QY 255 PPG-CWGC-----WQKHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGGVA- 301

Db 255 PPGRCRCRCPRLQLQAYSWKEEBE-----DEGSMEISLTSEGEPP-----GSEVVI 302

QY 302 -----SPTSSSGSSSRGT-ERPRSLKR-----GSKPSASSASLEKMKMVSQSFT 345

Db 303 KMPWVDSEAQAFTKQPKSSPNTVKRPTKKGDRGKGQKPRKE-QLAKR----- 352

QY 346 QRFLSRDRKVAKSIAVIVSIFGLCWAPYTLMIIRAAACHGHCVPDYWYETSFLLWANS 405

Db 353 KTFSLVKEKKAARTLSAILLAFILTWTPYINIMVLVSTFCK-DCVPETLWELGYLWCYVNS 411

QY 406 AVNPVLYPLCHHSFRRAFTKLL 427

Db 412 TVNPMCYALCNKAFRDTFRLLL 433

## RESULT 4

S09508

muscarinic acetylcholine receptor M1 - human

C:Species: Homo sapiens (man)

C&gt;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004

C:Accession: S09508; S06327; S04326

R:Chapman, C.G.; Browne, M.J.



A;Residues: 1-460 <SHA>  
A;Note: the authors translated the codon ATC for residue 119 as Thr  
R;Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.  
J. Biol. Chem. 264, 6596, 1989  
A;Reference number: A92742  
A;Contents: annotation; erratum, correct translation of residue 119  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospholipase A2; GPCR  
F;25-50/Domain: transmembrane #status predicted <TM1>  
F;62-93/Domain: transmembrane #status predicted <TM2>  
F;100-121/Domain: transmembrane #status predicted <TM3>  
F;142-168/Domain: transmembrane #status predicted <TM4>  
F;187-209/Domain: transmembrane #status predicted <TM5>  
F;367-387/Domain: transmembrane #status predicted <TM6>  
F;402-420/Domain: transmembrane #status predicted <TM7>  
  
Query Match 24.5%; Score 578; DB 2; Length 460;  
Best Local Similarity 33.0%; Pred. No. 2.7e-33;  
Matches 146; Conservative 68; Mismatches 150; Indels 78; Gaps 17;  
  
QY 33 W-TAVLAALMALLIVATVGLNVALMFLAVDSLSLTQNNFLLNLAIISDFLVGAFCDIPLY 91  
DB 23 WQAFIGSTGLSLATVGLNLLVLSIKVNTLKTANNVYFLLSLACADLIIGTFSMNLY 82  
  
QY 92 VYVLTGRWTFGRGLKMLVVDVLLCTSSAFNVLISVDRELSVTRAVSVRAQQDTRR 151  
DB 83 TTYLLMGHWLGTACDLMLALDYVNASVNNLLISFDRIYSVTRPLSVTRAKR-TPRR 141  
  
QY 152 AVRKMLLVVLAFLYPAILLSWEYLSGSSISPEGHGCAEFFYNYFLITASTLEFFTFP 211  
DB 142 AALMIGLAWLVSEVFWAPAILFQWLVGERTVLACQYIQFLSQIPIITFGTAAAFYLP- 200  
  
QY 212 LSVTFNLSIYLNQIRTRRLDGLAREAA--GPEPP-----PEAQSPPPP 254  
DB 201 --VTVM--CTLYWRIYRETNR---ARELAALQSGTTPGKGGSSSSRSOPGABGSPES 254  
  
QY 255 PPG-CWGC-----WQGHGEAMPLHRYGVGEAAVGEAEATLGGGGGGGVA- 301  
DB 255 PPGRCRCRAPRLLOAVSWKEEBE-----DEGSMESLTSSEGEPP-----GSEVVI 302  
  
QY 302 -----SPTSSGSSSROT-RRPSRLK-----GSKPSASSASLEKRMKMWVSQSFT 345  
DB 303 KMPWVDPEAQAPTKPPKSSPNTVKRTKGRDRGKGQKPRGK-QMAKR----- 352  
  
QY 346 QRFRLSRDRKVAKSLAVISIFGLCWAPYLLMITRAACHGCVDPDYWYETSFLLWANS 405  
DB 353 KTFSLVKEKAARTLSAILAFILTWPNIMVLVSTFCR-DCVPETLWELGYWLCYVNS 411  
  
QY 406 AVNPVLYPLCHHSFRRAFTKLL 427  
DB 412 TVNPMCYASCNAFRDHFLLLL 433  
  
RESULT 7  
muscarinic acetylcholine receptor m3 - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S47572  
R;Lee, P.H.K.; Hodges, P.K.; Glickman, F.; Chang, K.J.  
Biochim. Biophys. Acta 1223, 151-154, 1994  
A;Title: Cloning and expression of a cDNA encoding bovine muscarinic acetylcholine m3 re  
A;Reference number: S47572; MUID:194339178; PMID:8061048  
A;Accession: S47572  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-590 <LE>  
A;Cross-references: UNIPROT:P41984; EMBL:U08286; NID:G520465; PIDN:AAA51866.1; PID:G5204  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: neurotransmitter receptor  
  
Query Match 23.4%; Score 553.5; DB 2; Length 590;  
Best Local Similarity 27.1%; Pred. No. 1.8e-31;  
Matches 146; Conservative 68; Mismatches 150; Indels 78; Gaps 17;

Matches 149; Conservative 86; Mismatches 175; Indels 139; Gaps 18;  
  
QY 5 PPD-----GPLNASCALAGDAAAAGGAR----GFSAAWTAV-LAALMALLIVATVGLNVAL 54  
DB 30 PPGVTWTFHFGSYNISRA-AGNLSSPNGTSDPLGGHTIMQVVFIAFLTGLVALVTIIGNIL 88  
  
QY 55 VMLAFVADSSRTQNNFLLNLAIISDFLVGAFCDIPLYVYVYVLTGRWTFGRGLCKLWLVVD 114  
DB 89 VIVAFKVNKQKTVNNYFLLSLACADLIIGVSNLFTTYIIMRWALGNLACDLWLSID 148  
  
QY 115 YLLCTSSAFNVLISYDRFLSVTRAVSVRAQQDTRRVRKVLVWVLAFLYLPAILSW 174  
DB 149 YVASNASVNNLLVISFDRIYSITRPLTVTRAKR-TTKRAGVMIGLAWVISFILWAPAILFW 207  
  
QY 175 BYLSGSSISPEGHGCAEFFYNYFLITASTLEFFTFPLSVTFNLSIYLNQIRTRRLD 234  
DB 208 QYFVGKRTVPFGECFIQFLSEPTITFGTAIAAFYMPVTIMTILYWRIYKETEKRTRK-ELA 266  
  
QY 235 GARBAAGPEPPPEAQSPPPPFGWGC----- 261  
DB 267 GL-QASGTE--ABAEFNVHPTGSSRSYSELOQOSMRKRSARRKYGRCHFWFTTKSWRPS 323  
  
QY 262 -----WQGHGEAMPLHRYGVGEAAVGEAE-----GEAT----- 290  
DB 324 AEQMDQDHSSSDSMNNNDAAASLENSASSDEEDIGSETRAIYSLVILKLPGHSTILNKT 383  
  
QY 291 -----LGGG-----GGSV-----ASPT 304  
DB 384 PSSDNLQVPEELSGVLERKPSKLTQOQSDMGSGFQSKLPQLQIESAVDTAKASDV 443  
  
QY 305 SSSGSSSRGTRPRSLKRGSKPSASSASLEKRMKMWVSQ-FTORFLS--RDRKVAKSLA 361  
DB 444 NSSVGKTTAT-LPLSFK-----EATLAKRFAUKTSQITKRKMSLIEKKAAQQLS 494  
  
QY 362 VIVSIFGLCWAPYLLMITRAACHGCVDPDYWYETSFLLWANSVNPVLYPLCHHSFR 421  
DB 495 AILLAFIITWPNIMVLVNTFCD-CPKTYWNLGYWLCVINSTVNPVPCVLCNKTFRN 553  
  
QY 422 AFTKLLCQ 430  
DB 554 TFGMLLLCQ 562  
  
RESULT 8  
S01114  
muscarinic acetylcholine receptor M2, glandular - pig  
N;Alternate names: muscarinic acetylcholine receptor III  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C;Accession: S01114  
R;Akiba, I.; Kubo, T.; Maeda, A.; Bujo, H.; Nakai, J.; Mishina, M.; Numa, S.  
FEBS Lett. 235, 257-261, 1988  
A;Title: Primary structure of porcine muscarinic acetylcholine receptor III and antagonis  
A;Reference number: S01114; MUID:88296835; PMID:3402600  
A;Accession: S01114  
A;Molecule type: DNA  
A;Residues: 1-590 <AKI>  
A;Cross-references: UNIPROT:P11483; EMBL:X12712; NID:G1861; PIDN:CAA31215.1; PID:G1862  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmen  
F;68-91/Domain: transmembrane #status predicted <TM1>  
F;105-125/Domain: transmembrane #status predicted <TM2>  
F;143-164/Domain: transmembrane #status predicted <TM3>  
F;185-207/Domain: transmembrane #status predicted <TM4>  
F;231-252/Domain: transmembrane #status predicted <TM5>  
F;493-513/Domain: transmembrane #status predicted <TM6>  
F;528-546/Domain: transmembrane #status predicted <TM7>  
  
Query Match 23.1%; Score 546.5; DB 2; Length 590;  
Best Local Similarity 26.6%; Pred. No. 5.7e-31;  
Matches 146; Conservative 87; Mismatches 177; Indels 139; Gaps 17;  
  
QY 5 PPD-----GPLNASCALAGDAAAAGGAR----GFSAAWTAV-LAALMALLIVATVGLNVAL 54

Db 30 PPGTWHFGSYNISQA-AGNFSPNGTSDPLGGHTIWOVVFIAFTGLALVTIIGNIL 88  
Qy 55 VMLAFVADSSLRQNNFLLNLAIISDFLVGAFCIPLYPYVLTGRWTFGRGLCKLWLVD 114  
Db 89 VIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMNLTFTYIIMRWALGNLACDLWLAD 148  
Qy 115 YLLCTSSAFNVLISYDRFLSVTRAVSVRAOQDTRRAVRKMLLVWVLAFLYGPAILSW 174  
Db 149 VYASNASVNNLVISFDRYFSITRPLTYRAKR-TTKRAGVMIGLAWISFVLWAPAILFW 207  
Qy 175 EYLSGSSSIPEGHGCAEFPYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRRLRLD 234  
Db 208 QYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYMPVTIMTILYWRKYKTEKRTK-ELA 266  
Qy 235 GAREAAAGPEPPPEAOPSPPPPGCGWC----- 261  
Db 267 GL-QASGTE--AEENFVHPTGSSRSCSYELOQSLKRSARKYGRCHFVFTTWSKPS 323  
Qy 262 -----WQKGHEAMPLHRYGVGEAAVGAEA-----GEATLGG----- 294  
Db 324 AEQMDQDHSSSDSWNNDAASLENSASDEEDIGSETRAIYSIVLKLPGHSTILNSTKL 383  
Qy 295 -----GGGGSV-----ASPT 304  
Db 384 PSSDNLQVPEELGTVDLERKASKLQAQKSMDDGGSFQSKLPQLQLESADVDTAKASDV 443  
Qy 305 SSSGSSSRTERPSRLKRGSKPSASSASLEKMKMVQS--FTQPRLS--RDRKVAKSLA 361  
Db 444 NSSVKKTAT-LPLSFK-----EATLAKFALKTRSQITKRKMSLVKKEKAAQTLS 494  
Qy 362 VIVSIFGLCWAPYTLMIIRAACHGCHVDYNYETSFWLLWANSVAVNPVLYPLCHHSFR 421  
Db 495 ALLAFIITWTYNNVLVNTFCDS-CIPKTYNGLWLYCYNSTVNPVYALCNKTFRT 553  
Qy 422 APTKLLCPQ 430  
Db 554 TFKMLLLCQ 562

RESULT 9  
S10128  
muscarinic acetylcholine receptor M4 - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C:Accession: S10128  
R:Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A>Title: Distinct primary structures, ligand-binding properties and tissue-specific expression of two human muscarinic acetylcholine receptor cDNAs  
A:Reference number: S04326; MUID:88166632; PMID:3443095  
A:Accession: S10128  
A:Molecule type: DNA  
A:Residues: 1-590 <PER>  
A:Cross-references: UNIPROT:P20309; EMBL:X15266; NID:g32323; PIDN:CAA33337.1; PID:g32324  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; rhodopsin  
F:68-95/Domain: transmembrane #status predicted <TM1>  
F:105-131/Domain: transmembrane #status predicted <TM2>  
F:143-164/Domain: transmembrane #status predicted <TM3>  
F:185-207/Domain: transmembrane #status predicted <TM4>  
F:231-252/Domain: transmembrane #status predicted <TM5>  
F:493-513/Domain: transmembrane #status predicted <TM6>  
F:525-546/Domain: transmembrane #status predicted <TM7>  
F:5,6,15,41/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 22.9%; Score 541; DB 2; Length 590;  
Best Local Similarity 26.2%; Pred. No. 1.4e-30;  
Matches 145; Conservative 88; Mismatches 178; Indels 142; Gaps 18;  
Qy 5 PPD-----GPLNASGALAGDAAGAR-----GFSNAWTAVALAALMALLIVATVILGNAL 54  
Db 30 PPGTWHFGSYNVSRA-AGNFSPDGTDDPLGGHTVQVVFIAFTGLALVTIIGNIL 88

Qy 55 VMLAFVADSSLRQNNFLLNLAIISDFLVGAFCIPLYPYVLTGRWTFGRGLCKLWLVD 114  
Db 89 VIVAFKVNKQLKTVNNYFLLSLACADLIIGVISMNLTFTYIIMRWALGNLACDLWLAD 148  
Qy 115 YLLCTSSAFNVLISYDRFLSVTRAVSVRAOQDTRRAVRKMLLVWVLAFLYGPAILSW 174  
Db 149 VYASNASVNNLVISFDRYFSITRPLTYRAKR-TTKRAGVMIGLAWISFVLWAPAILFW 207  
Qy 175 EYLSGSSSIPEGHGCAEFPYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRRLRLD 234  
Db 208 QYFVGKRTVPPGECFIQFLSEPTITFGTAIAAFYMPVTIMTILYWRKYKTEKRTK-ELA 266  
Qy 235 GAREAAAGPEPPPEAOPSPPPPGCGWC----- 261  
Db 267 GL-QASGTE--AEENFVHPTGSSRSCSYELOQSLKRSARKYGRCHFVFTTWSKPS 323  
Qy 262 -----WQKGHEAMPLHRYGVGEAAVGAEA-----GEATLGG----- 294  
Db 324 AEQMDQDHSSSDSWNNDAASLENSASDEEDIGSETRAIYSIVLKLPGHSTILNSTKL 383  
Qy 295 -----GGGGSV-----ASPT 304  
Db 384 PSSDNLQVPEELGTVDLERKASKLQAQKSMDDGGSFQSKLPQLQLESADVDTAKASDV 443  
Qy 305 SSSGSSSRTERPSRLKRGSKPSASSASLEKMKMVQS--FTQPRLS--RDRKVAKSLA 361  
Db 444 NSSVKKTAT-LPLSFK-----EATLAKFALKTRSQITKRKMSLVKKEKAAQTLS 494  
Qy 362 VIVSIFGLCWAPYTLMIIRAACHGCHVDYNYETSFWLLWANSVAVNPVLYPLCHHSFR 421  
Db 495 ALLAFIITWTYNNVLVNTFCDS-CIPKTYNGLWLYCYNSTVNPVYALCNKTFRT 553  
Qy 422 APTKLLCPQ 431  
Db 554 TFKMLLLCQ 566  
RESULT 10  
B29514  
muscarinic acetylcholine receptor M3 - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 09-Jul-2004  
C:Accession: B94518; B94293; B37121; B29514  
R:Bonner, T.I.  
submitted to GenBank, July 1987  
A:Reference number: A94518  
A:Accession: B94518  
A:Molecule type: mRNA  
A:Residues: 1-589 <BO1>  
A:Cross-references: UNIPROT:P08483  
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.  
Science 237, 527-532, 1987  
A>Title: Identification of a family of muscarinic acetylcholine receptor genes.  
A:Reference number: A94293; MUID:87263421; PMID:3037705  
A:Accession: B94293  
A:Molecule type: mRNA  
A:Residues: 1-269; 463-589 <BO2>  
A:Experimental source: cerebral cortex  
A>Note: only a part of the protein translation is given; none of the nucleotide sequence  
R:Kurtzsch, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.  
J. Biol. Chem. 265, 13702-13708, 1990  
A>Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues involved in binding of [3H]muscimol and [3H]nicotine  
A:Reference number: A37121; MUID:90337982; PMID:2380182  
A:Accession: B37121  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 104-166 <KUR>  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transmembrane protein; rhodopsin  
F:67-90/Domain: transmembrane #status predicted <TM1>  
F:104-124/Domain: transmembrane #status predicted <TM2>  
F:142-163/Domain: transmembrane #status predicted <TM3>  
F:184-206/Domain: transmembrane #status predicted <TM4>

F;230-251/Domain: transmembrane #status predicted <TM5>  
F;492-512/Domain: transmembrane #status predicted <TM6>  
F;527-545/Domain: transmembrane #status predicted <TM7>  
F;6,15,41,48,52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.8%; Score 539; DB 2; Length 589;  
Best Local Similarity 26.2%; Pred. No. 1.9e-30;  
Matches 135; Conservative 83; Mismatches 103; Indels 130; Gaps 14;

QY 28 GFSAAMTAV-LAALMALLIVATVGLNALVMFAVDSSRLRTONFFLLNLAIISDFLVGAF 86  
DB :  
Db 60 GGHTIQVFIFAEFTGFALVTIIGHILVIVAFVKVKQLKTNNYIFLLSLACADLIIGVI 119  
QY 87 CIPLYPYVPVLGRWTFEGRGCKLWLVDYLCTSSAFNVLISYDRFLSVTRAVSRAOQ 146  
DB :  
Db 120 SMLNFTTYIIIMRWALGNCLDWLSIDYVASNAVMNLIVISFDRYFSITRPLTYRAKR 179  
QY 147 GDTRRAVRKMLVVWLAFLLYGPAILSWELSGSSIPEGHCVAEFPFNWYFLITASTLE 206  
DB :  
Db 180 TTKRRGV-MIGLAWVISFVLWAPAILFWQYFGKRTVPPGCEFIQLSEPTITFTGTAA 238  
QY 207 FETPFLSVTFNLSIYNLTQRRLRLDGAAGPEPPEAQSPPPPCCWGCG----- 261  
DB :  
Db 239 FYMPVTIMTLYWRIYKETEKRYK-ELAGL-QASGTE--AEAENFVHPGSSRS CSSYEL 294  
QY 262 -----WQKHGEAMPLHYRGVGEA 280  
DB :  
Db 295 QQQGVKSRKKYGRCHFNFPTTSKWPSAEQMDDHSSSDSNNDAAASSENSASDEE 354  
QY 281 AVQAEE-----GSATLG 292  
DB :  
Db 355 DIGSETRAIYSIVLKLPGHSSILNSTKLPSDDLQVSNEDLGTVDVVERNAHKLQAOKSMG 414  
QY 293 GGGG-----GGVASPTSSGSSRGTERPRSLKRGSKPSASSASLEKR 336  
DB :  
Db 415 DGNCKODFKLPFOLESADVDTGKTDSTNSSADKTTAT-LPLSFK-----EATLAKR 465  
QY 337 MNKVQS-FQRPRLS--RDRKVAKSIAVIVSIFGLCWAPYTLLMIIRAACHGCVCVPDYR 393  
DB :  
Db 466 FALKTRSQTIKRKEMSLIKEKAQILSALLAFIITWTPYINIMVLVNTFCDS-CIPKY 524  
QY 394 YETSFWLLWANSANPVLPCHHSFRRAF-TKLLC 428  
DB :  
Db 525 WNLGYWLCVINSTVNPCVALCNKTFRTFKTLLOC 560

RESULT 11  
S10127  
muscarinic acetylcholine receptor M3 - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S10127  
R;Berlatta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramachandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expression patterns of three members of the muscarinic acetylcholine receptor family  
A;Reference number: S04326; MUID:88166632; PMID:3443095  
A;Accession: S10127  
A:Molecule type: DNA  
A;Residues: 1-479 <PER>  
A;Cross-references: UNIPROT:P081173; EMBL:X15265; NID:g32321; PID:g32322  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatase  
F;32-57/Domain: transmembrane #status predicted <TM1>  
F;70-94/Domain: transmembrane #status predicted <TM2>  
F;106-128/Domain: transmembrane #status predicted <TM3>  
F;148-171/Domain: transmembrane #status predicted <TM4>  
F;192-216/Domain: transmembrane #status predicted <TM5>  
F;401-422/Domain: transmembrane #status predicted <TM6>  
F;433-456/Domain: transmembrane #status predicted <TM7>  
F;3,8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.7%; Score 536; DB 2; Length 479;  
Best Local Similarity 25.6%; Pred. No. 2.5e-30;

Db 66 NNYFLSGLACADLIIGAFSMNLYTYIIKGYWPLGAVVCDLWLDYVVSASVNNLLII 125

Qy 129 SYDRFLSVTRAVSVRAOQDTRRAVRKMLLVWVLAFLLYGPAILSWELSGSSSIPEGHC 188

Db 126 SFDRYFCVTKPLTYPAR--TTKAGLMTAAAWLSFVLWAPAILFWQFVVGKRTVPDNOQ 184

Qy 189 YAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRL---RLDGAREAAAG--- 241

Db 185 FIOFLSNPAVTFGTAAIAAFYLPVVMITV--LYIHISLASRSRVHKKRPEGPKAKATLA 242

Qy 242 -----PEPPP-----EAQSP--PPPGCGWCWKHGEAMPLHRY 275

Db 243 FLKSPLMKPSIKKPPPGGASREELRNGKLEBAPPALPPPP----- 283

Qy 276 GVGEAAVGAEGEATLGGGGGGSVASPTSSSGSSSRGTE-----RPRSLKRGSKPS- 327

Db 284 --RPVADKDTSNESSGSATQNTKERPPTELSTTEAATTPALPTLPRTLPNPAKWSK 341

Qy 328 -----ASSASLEKRMKWVSQSFTQFR--LSRDRKVAKS 359

Db 342 IQIVTKQTGSECVTAIEIVPATPGMRPAANVARKFASIAARNVKKRQMAARERKVTRT 401

Qy 360 LAVIVSIFGLCWAPYLLMIIRAACHGVDPDYWTETSFVLLWANSVNPVLYPLCHHSF 419

Db 402 IFAILLAFILTWTPYNNVMLVNTFCQS--CIPERVWSIGYMLCYVNSTINPACYALCNATF 460

Qy 420 RRAFTKLCPQ 430

Db 461 KKTFRHLLLCQ 471

RESULT 13

C29514

muscarinic acetylcholine receptor M4 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 24-Nov-1999

C:Accession: C94518; C94293; E37121; C29514

R:Bonner, T.I.

submitted to GenBank, July 1987

A:Reference number: A94518

A:Accession: C94518

A:Molecule type: mRNA

A:Residues: 1-478 <BOI>

R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.

Science 237, 527-532, 1987

A:Title: Identification of a family of muscarinic acetylcholine receptor genes.

A:Reference number: A94293; MUID:87263421; PMID:3037705

A:Accession: C94293

A:Molecule type: mRNA

A:Residues: 1-233;373-478 <BO2>

A:Experimental source: cerebral cortex

A:Note: only a part of the protein translation is given; none of the nucleotide sequence

R:Kurtenbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.

J. Biol. Chem. 265, 13702-13708, 1990

A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo

A:Reference number: A37121; MUID:90337982; PMID:2380182

A:Accession: E37121

A>Status: preliminary

A:Molecule type: protein

A:Residues: 68-130 <KUR>

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:106-127/Domain: transmembrane #status predicted <TM3>

F:147-170/Domain: transmembrane #status predicted <TM4>

F:192-215/Domain: transmembrane #status predicted <TM5>

F:401-421/Domain: transmembrane #status predicted <TM6>

F:433-454/Domain: transmembrane #status predicted <TM7>

F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.6%; Score 532.5; DB 2; Length 478;

Best Local Similarity 25.1%; Pred. No. 4.4e-30;

Matches 127; Conservative 96; Mismatches 158; Indels 125; Gaps 12;

Qy 9 PLNAGSALGADAAAAGGARGFSAATVLAALMALLIVATVGLNALVMLAFVADSLRQ 68

Db 6 PVNGSSANQSVRLVTAAHNHLETVEWFIATVTGSLSLVTVVGNIILVMSIKVNRLOQTV 65

Qy 69 NNPFLNLIAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLI 128

Db 66 NNYFLSGLCADLIIGAFSMNLYTYIIKGYWPLGAVVCDLWLDYVVSASVNNLLII 125

Qy 129 SYDRFLSVTRAVSVRAOQDTRRAVRKMLLVWVLAFLLYGPAILSWELSGSSSIPEGHC 188

Db 126 SFDRYFCVTKPLTYPAR--TTKAGLMTAAAWLSFVLWAPAILFWQFVVGKRTVPDNOQ 184

Qy 189 YAEFFYNWYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRL---RLDGAREAAAG--- 241

Db 185 FIOFLSNPAVTFGTAAIAAFYLPVVMITV--LYIHISLASRSRVHKKRPEGPKAKATLA 242

Qy 242 -----PEPPP-----EAQSP--PPPGCGWCWKHGEAMPLHRY 275

Db 243 FLKSPLMKPSIKKPPPGGASREELRNGKLEBAPPALPPPP-----RPVP----- 287

Qy 276 GVGEAAVGAEGEATLGGGGGGSVASPTSSSGSSSRGTE----- 315

Db 288 -----DKDTSNENSSSGSATQNTKERPPTELSTTEAATTPALPAP 325

Qy 316 --RPRSLKRGSKPS-----ASSASLEKRMKWVSQSFTQ 346

Db 326 TLQPTLPNPAKWSKIQIVTKQTGNECVTAIEIVPATPGMRPAANVARKFASIAARNQVR 385

Qy 347 RFR--LSRDRKVAKS LAVIVSIFGLCWAPYLLMIIRAACHGVDPDYWTETSFVLLWANS 404

Db 386 KKRQMAARERKVTRTIFAILLAFILTWTPYNNVMLVNTFCQS--CIPETVWSIGYMLCYVN 444

Qy 405 SAVNPVLYPLCHSFRRAFTKLCPQ 430

Db 445 STINPACYALCNATFKKTRHLLLCQ 470

RESULT 14

JT0530

muscarinic acetylcholine receptor M5 - human

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 21-Jan-2000

C:Accession: JT0530

R:Bonner, T.I.; Young, A.C.; Brann, M.R.; Buckley, N.J.

Neuron 1, 403-410, 1988

A:Title: Cloning and expression of the human and rat m5 muscarinic acetylcholine receptor

A:Reference number: JT0530; MUID:90166521; PMID:3272174

A:Accession: JT0530

A:Molecule type: DNA

C:Residues: 1-532 <BON>

C:Comment: Muscarinic acetylcholine receptors mediate many of the actions of the neurotr

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho

F:30-53/Domain: transmembrane #status predicted <TM1>

F:67-87/Domain: transmembrane #status predicted <TM2>

F:105-126/Domain: transmembrane #status predicted <TM3>

F:147-169/Domain: transmembrane #status predicted <TM4>

F:192-214/Domain: transmembrane #status predicted <TM5>

F:444-464/Domain: transmembrane #status predicted <TM6>

F:479-498/Domain: transmembrane #status predicted <TM7>

F:8,13/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.3%; Score 527.5; DB 2; Length 532;

Best Local Similarity 27.4%; Pred. NO. 1.1e-29;

Matches 139; Conservative 79; Mismatches 165; Indels 125; Gaps 15;

Qy 33 WTAV-LAALMALLIVATVGLNALVMLAFVADSSLRTQNNFFLLNLAISDFLVGAFICPLY 91

Db 28 WEVITIAAVTAVSLITIVGNVLMSPKVNSQLNPNYVLLSLACADLIISGIFSMNLY 87

Qy 92 VPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNIVLISYDRFLSVTRAVSVRAOQDTRR 151



```
Db      88  TTYILMGRWALGSLADLWLDYVNASVNMNLIVISFDYFESITRPLTYRAKE-TPKR 146
QY      152  AVRKMLLVWVLAFLYGAILLSWEYLSGSSIPDEGHCAVEFFYNNWYFLITASTLEFFTPF 211
Db      147  AGIMIGLAWLISFILWAPAILCWQVLGKRTVPLDECOIQLSEPTITFGTAIAAFYIPV 206
QY      212  LSVTFNLSIYLNIQRRTR--LRLDGA----- 236
Db      207  SVMTILYCRIRYRETKRYKLDADLOGSDSVTKAEKRAKPAHRALFRSCLURCPRTLAQER 266
QY      237  -----REAGGP-----PPPEAQSPPPPPPGCWGCWQ 263
Db      267  NQASWSSRRSTSTTGKFSQATGPSANWAKAEQLTTCSSYPSSSEDEKPAITDPLVLQVYV- 325
QY      264  KGHGEAMPLHRYGVGEAAVGAEBATLGGGGGGSVASPTSSSG-----SSRGTER 316
Db      326  KSQKESP-----GE-BFSAETEETF-----VKAETEKSDYDTPNYLLSPAAHR 370
QY      317  PRSLK-----RGSK-----PSASSASLEKRMKVQSQSFOTRF 348
Db      371  PAKQKVAIKFRLVKAQNGETNNGCHKVKIMPCFPFVAKPEPSTKGLNPNPSHQMTARK 430
QY      349  R--LSRDRKVAKSLAVIYSIFGLCWAPYTLMIIRAACHGCVDPDYWYETSFWLLWANS 406
Db      431  RWLVKERAQAQLSAILLAFIITWTPYNIMVLVSTFC-DKCPVPTLWHLGVWLCYVNST 489
QY      407  VNPVLYPLCHHSFRRAFTK-LLCPQKLK 433
Db      490  VNPICVYALCNTRFKRTFRKMLLCRWKK 517
```

## RESULT 15

```
JH0197
muscarinic acetylcholine receptor M2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 24-Nov-1999
C:Accession: JH0197; D37121
R:Jai, J.; Bloom, J.W.; Yamamura, H.I.; Roeske, W.R.
Life Sci. 47, 1001-1013, 1990
A:Title: Amplification of the rat m2 muscarinic receptor gene by the polymerase chain re
A:Reference number: JH0197; PMID:91041524; PMID:2172674
A:Accession: JH0197
A:Molecule type: DNA
A:Residues: 1-466 <LAI>
R:Kurtendach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C.
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues invo
A:Reference number: A37121; PMID:90337982; PMID:2380182
A:Accession: D37121
A>Status: preliminary
A:Molecule type: protein
A:Residues: 60-122 <KUR>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; transme
F:23-48/Domain: transmembrane #status predicted <TM1>
F:61-85/Domain: transmembrane #status predicted <TM2>
F:98-119/Domain: transmembrane #status predicted <TM3>
F:139-162/Domain: transmembrane #status predicted <TM4>
F:184-207/Domain: transmembrane #status predicted <TM5>
F:389-409/Domain: transmembrane #status predicted <TM6>
F:421-442/Domain: transmembrane #status predicted <TM7>
```

```
Query Match      22.3%; Score 525.5; DB 2; Length 466;
Best Local Similarity 26.8%; Pred. No. 1.3e-29;
Matches 130; Conservative 94; Mismatches 170; Indels 91; Gaps 12;

QY      11  NASGALAGDAAGARGFSAAWTAVLAALMALLIVATVLGNALVLAFAVDSSLRTONN 70
Db      3  NSTNSNNGLAITSYKTFEVVIVLVAGSLV---TIGNILWVSVKVRHLQTVNN 59
QY      71  FFLNLALISDFLAVGAFICPLYVYPVYLTGRWTFGRGLCKLWLWVYLLCTSSAFNIVLISY 130
```

```
Db      60  YFLSFLACADLIIGVFSNMNLYTLTVIGYWPPLGPVVCWLWLALDYVSNASVMNLLIISF 119
QY      131  DRFLSVTPAVSYRAQOGDTRAVRKMLLVWLAFLLYCPAILLSWELSGGSSIPGHCVYA 190
Db      120  DRYFCVTKPLTYPKR-TTKWAGMMIAAAWVLSFILWAPAILFWQFIVGVRTVEGECYI 178
QY      191  EFFYNNWYFLITASTLEFFTPFSLSVTFNLSIYLNIQRRTRLRLDGAREAAAGPEPPPEAQ 250
Db      179  QFFSNAVTFGTAAAFVLPVIMTV-----LYWHISRAKSKRIKEKK-----EPVANO 228
QY      251  SPPPPPGCWGCWQKHGGEAMP-----LHRYGVGEAAVGAEEA----- 289
Db      229  DPVSPSLVQGRIVKPNNNMPPGGGLEHKNKIQNGKAPRDGVTENCVOGEEKSESSNDSTS 288
QY      290  -----TLGGG-----GGGGSVASPTSSS-----G 308
Db      289  VSAVASNNRRDDEITQDENTVSTSLGSHRDDNSKQTCIKIVTKAQKGDVYTPSTTTVELVG 348
QY      309  SSSR-GTERPRSLKRGSKPSASSASLEKRMKVQSQSFQRFRLSRDRKVAKSLAVIVSIF 367
Db      349  SSGQNGDEKQNIAR-----KIVKTKQPAKKKPPPSREKKVTRTILAILLAF 396
QY      368  GLCWAPYTLMIIRAACHGCVDPDYWYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLL 427
Db      397  IITWAPYNNVMVLINTFC-APCIPNTVWTIGYWLVCYINSTINPACVYALCNATFKTKFKHLL 455
QY      428  -CPQK 431
Db      456  MCHYK 460
```

Search completed: June 2, 2005, 20:41:15

Job time : 26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 14:45:59 ; Search time 83 Seconds  
(without alignments)  
2745.485 Million cell updates/sec

Title: US-10-727-021-7

Perfect score: 2361  
Sequence: 1 MERAPPDGLNAGALGDA.....LLCPQKLIKPHSSLEHCWK 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2357	99.8	445	1 HH3R_HUMAN	Q9Y5N1 homo sapien
2	2323	98.4	445	2 Q865E1	Q865E1 macaca mulla
3	2320	94.0	445	1 HH3R_MOUSE	P58406 mus musculus
4	2213	93.7	445	1 HH3R_RAT	Q9GYN8 rattus norv
5	2179	92.3	445	1 HH3R_CAVPO	Q9J135 cavia porce
6	1919	81.3	365	2 Q8WY01	Q8WY01 homo sapien
7	1919	81.3	373	2 Q8WXZ9	Q8WXZ9 homo sapien
8	1521	64.4	301	2 Q8WY00	Q8WY00 homo sapien
9	1521	64.4	309	2 Q8N149	Q8N149 homo sapien
10	1233	51.8	247	2 Q8K116	Q8K116 mus musculus
11	1186	50.2	473	2 Q6ZM33	Q6ZM33 brachydanio
12	1137	48.2	210	2 Q8NCH4	Q8NCH4 homo sapien
13	860	36.4	200	2 Q8N150	Q8N150 homo sapien
14	754	31.9	147	2 Q865E3	Q865E3 canis famil
15	724	30.7	390	1 HH4R_HUMAN	Q9H3N8 homo sapien
16	724	30.7	390	2 Q961D9	Q961D9 homo sapien
17	723	30.6	391	2 Q91ZY2	Q91ZY2 mus musculus
18	703	29.8	391	2 Q91ZY1	Q91ZY1 rattus norv
19	694.5	29.4	390	2 Q8WNV9	Q8WNV9 sus scrofa
20	688.5	29.2	389	2 Q91ZY3	Q91ZY3 cavia porce
21	592.5	25.1	460	1 ACW1_MACMU	P56489 macaca mulla
22	592	25.1	460	1 ACW1_RAT	P08482 rattus norv
23	591.5	25.1	454	2 Q96RH1	Q96RH1 homo sapien
24	591.5	25.1	460	1 ACW1_HUMAN	P11229 homo sapien
25	587.5	24.9	460	1 ACW1_PIG	P04761 sus scrofa
26	580	24.6	458	2 Q8VH28	Q8VH28 cavia porce
27	580	24.6	460	1 ACW1_MOUSE	P12657 mus musculus
28	570	24.1	110	2 Q865E2	Q865E2 canis famil
29	564	23.9	530	2 Q8VH24	Q8VH24 cavia porce
30	553.5	23.4	590	1 ACW3_BOVIN	P41984 bos taurus
31	548.5	23.2	528	2 Q9PTF6	Q9PTF6 gallus gall

#### RESULT 1

ID	HH3R_HUMAN	STANDARD;	PRT;	445 AA.
AC	Q9Y5N1: Q9GZX2: Q9H4K8;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DE	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Histamine H3 receptor (HH3R) (G protein-coupled receptor 97) .			
GN	Name=HRH3; Synonyms=GPCR97;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	TISSUE=Thalamus;			
RX	MEDLINE=20568725; PubMed=10347254;			
RA	Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,			
RA	Huvar A., Jackson M.R., Erlander M.G.;			
RT	"Cloning and functional expression of the human histamine H3			
RT	receptor.";			
RL	Mol. Pharmacol. 55:1101-1107(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.			
RX	MEDLINE=20568725; PubMed=1118334; DOI=10.1006/bbr.2000.4008;			
RA	Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;			
RT	"Molecular cloning and characterization of a new human histamine			
RT	receptor, HH4R.";			
RL	Biochem. Biophys. Res. Commun. 279:615-620(2000).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).			
RC	TISSUE=Thalamus;			
RX	MEDLINE=21181559; PubMed=11284713; DOI=10.1042/0264-6021:3550279;			
RA	Coge P., Guenin S.-P., Audinot V., Renouard-Tray A., Beauverger P.,			
RA	Macia C., Ouyri C., Nagel N., Riquie H., Boutin J.A., Galizzi J.-P.;			
RT	"Genomic organization and characterization of splice variants of the			
RT	human histamine H3 receptor.";			
RL	Biochem. J. 355:279-288(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME			
RC	VAL=280.			
RC	TISSUE=Blood;			
RX	MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s00702000036;			
RA	Wiedemann P., Boenisch H., Oerters F., Brues M.;			
RT	"Structure of the human histamine H3 receptor gene (HRH3) and			
RT	identification of naturally occurring variations.";			
RL	J. Neural Transm. 109:443-453(2002).			
RN	[5]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RA	Ullmer C., Zirwes E., Lubbert H.;			
RT	"Cloning and functional expression of the human histamine H3S			
RT	receptor.";			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

32	546.5	23.1	590	1	ACW3_PIG	P11483 sus scrofa
33	545	23.1	500	2	Q66LI8	Q66LI8 fugu rubrip
34	543	23.0	490	2	Q7T286	Q7T286 brachydanio
35	541	22.9	590	1	ACW3_HUMAN	P20309 homo sapien
36	541	22.9	590	1	ACW3_PANTR	Q9N2A4 pan troglod
37	540.5	22.9	590	1	ACW3_PONPY	Q9N2A2 pongo pygma
38	540	22.9	590	1	ACW3_GORGO	Q9N2A3 gorilla gor
39	539.5	22.9	564	2	Q96RG9	Q96RG9 homo sapien
40	538	22.8	589	1	ACW3_RAT	P08483 rattus norv
41	536.5	22.7	477	2	Q8VH25	Q8VH25 cavia porce
42	536	22.7	474	2	Q96RG8	Q96RG8 homo sapien
43	536	22.7	479	1	ACW4_HUMAN	P08173 homo sapien
44	535	22.7	479	1	ACW4_MOUSE	P32111 mus musculus
45	533.5	22.6	532	1	ACW5_MACMU	P56490 macaca mulla

#### ALIGNMENTS



```
Db 1 MERAPPDGPLNASGALAGEAAAGARGFSAANTAVLAALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRQTQNNFFLLNLAIISDFLVGAFICPLVYPVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRQTQNNFFLLNLAIISDFLVGAFICPLVYPVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLSYDRFLSVTRAVSVRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
Db 121 SAFNIVLSYDRFLSVTRAVSVRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYABFFNNYFLITASTLEFFTPFLSVTFNFNLSIYLNTOQRTLRDLGAREAA 240
Db 181 SSIPGHCYABFFNNYFLITASTLEFFTPFLSVTFNFNLSIYLNTOQRTLRDLGAREAA 240
QY 241 GPEPPEAQPPPPPPGCGWQKGHEAMPLHRYGVGEAAVGAAGBATLGGGGGGGSV 300
Db 241 GPEPPEAQPPPPPPGCGWQKGHEAMPLHRYGVGEAAVGAAGBATLGGGGGGGSV 300
QY 301 ASPTSSSSSSSGRTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360
Db 301 ASPTSSSSSSSGRTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMLIRAAACHGCVDPVYVYETSFWLLWANSVAVNPVLYPLCHHSFR 420
Db 361 AVIVSIFGLCWAPYTLMLIRAAACHGCVDPVYVYETSFWLLWANSVAVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCQKLIKIPHSLSHCWK 445
Db 421 RAFTKLLCQKLIKIPHSLSHCWK 445

RESULT 2
ID Q865E1 PRELIMINARY; PRT; 445 AA.
AC Q865E1;
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Histamine receptor H3.
GN Name=HRH3;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Yao B.B., Sharma R., Caesar S., Ebsenshade T.A., Hancock A.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AY231164; AA063757.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 445 AA; 48591 MW; E7940A4EC09CA8C CRC64;

Query Match
Best Local Similarity 98.4%; Score 2323; DB 2; Length 445;
Matches 437; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MERAPPDGPLNASGALAGEAAAGARGFSAANTAVLAALMALLIVATVGLNALVMLAFV 60
|||||
```

```
Db 1 MERAPPDGPLNASGALAGEAAAGARGFSAANTAVLAALMALLIVATVGLNALVMLAFV 60
QY 61 ADSSLRQTQNNFFLLNLAIISDFLVGAFICPLVYPVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRQTQNNFFLLNLAIISDFLVGAFICPLVYPVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNIVLSYDRFLSVTRAVSVRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
Db 121 SAFNIVLSYDRFLSVTRAVSVRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYABFFNNYFLITASTLEFFTPFLSVTFNFNLSIYLNTOQRTLRDLGAREAA 240
Db 181 SSIPGHCYABFFNNYFLITASTLEFFTPFLSVTFNFNLSIYLNTOQRTLRDLGAREAA 240
QY 241 GPEPPEAQPPPPPPGCGWQKGHEAMPLHRYGVGEAAVGAAGBATLGGGGGGGSV 300
Db 241 GPEPPEAQPPPPPPGCGWQKGHEAMPLHRYGVGEAAVGAAGBATLGGGGGGGSV 300
QY 301 ASPTSSSSSSSGRTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360
Db 301 ASPTSSSSSSSGRTERPRSLKRGSKPSASASLEKRMKMWVSQSFQRFSLRDRKVAKSL 360
QY 361 AVIVSIFGLCWAPYTLMLIRAAACHGCVDPVYVYETSFWLLWANSVAVNPVLYPLCHHSFR 420
Db 361 AVIVSIFGLCWAPYTLMLIRAAACHGCVDPVYVYETSFWLLWANSVAVNPVLYPLCHHSFR 420
QY 421 RAFTKLLCQKLIKIPHSLSHCWK 445
Db 421 RAFTKLLCQKLIKIPHSLSHCWK 445

RESULT 3
ID HH3R MOUSE STANDARD; PRT; 445 AA.
AC P59406;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN Name=Hrh3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1;
RA Coge F., Rigue H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,
RA Galizzi J.-P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
CC histamine signals in CNS and peripheral nervous system. Signals
CC through the inhibition of adenylylate cyclase and displays high
CC constitutive activity (spontaneous activity in the absence of
CC agonist) (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AY044153; AAK72406.1; -.
CC MGD; MGI:2139279; Hrh3.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR000390; H3_receptor.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRRHODOPSN.

DR EMBL; AY044153; AAK72406.1; -.
DR MGD; MGI:2139279; Hrh3.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR InterPro; IPR000390; H3_receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
```

```
DR PRINTS: PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G PROTEIN RECP F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 39 Extracellular (Potential).
FT TRANSMEM 40 60 Potential.
FT DOMAIN 61 70 Cytoplasmic (Potential).
FT TRANSMEM 71 91 Potential.
FT DOMAIN 92 108 Extracellular (Potential).
FT TRANSMEM 109 129 Potential.
FT DOMAIN 130 156 Cytoplasmic (Potential).
FT TRANSMEM 157 177 Potential.
FT DOMAIN 178 196 Extracellular (Potential).
FT TRANSMEM 197 217 Potential.
FT DOMAIN 218 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT DOMAIN 381 396 Extracellular (Potential).
FT TRANSMEM 397 417 Potential.
FT DOMAIN 418 445 Cytoplasmic (Potential).
FT TRANSMEM 446 465 Potential.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 445 AA; 48S41 MW; B8D406E29E1F3C5F CRC64;

Query Match 94.0%; Score 2220; DB 1; Length 445;
Best Local Similarity 93.9%; Pred No. 1.7e-118;
Matches 419; Conservative 8; Mismatches 17; Indels 2; Gaps 2;

QY 1 MERAPDPGLNAGALAGDAAGGARGFSAATVLAALMALLIVATVLGNALVMLAFV 60
DB 1 MERAPDPGLNAGALAGDAAGGARGFSAATVLAALMALLIVATVLGNALVMLAFV 60
QY 61 ADSSLRQNNFLLNLATSDFLVGFACIPLYVPYVLTGTWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRQNNFLLNLATSDFLVGFACIPLYVPYVLTGTWTFGRGLCKLWLVVDYLLCAS 120
QY 121 SAFNVLISYDFLSVTRAVSRAOQDTRRAVRKMLLWVLAFLLYGPAILSWELSGG 180
DB 121 SVFNVLISYDFLSVTRAVSRAOQDTRRAVRKMLWVLAFLLYGPAILSWELSGG 180
QY 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRLRDGLAREAA 240
DB 181 SSIPGHCYAEFFYNNYFLITASTLEFFTPFLSVTFNLSIYLNIOQRTRLRDGLGRE-A 239
QY 241 GPEPPEAQPSPPP-PPGCGWGWQKHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299
DB 240 GPEPPEAQPSPPPAPPSCWGCWPKHGEAMPLHRYGVGEAGPGVETGEAGLGGGGGGGA 299
QY 300 VASPTSSSSSSRGTERPRSLKRGSKPSSASSASLEKRMKWWSQSFTQRFRLSRDRKVAKS 359
DB 300 AASPTSSSSSSRGTERPRSLKRGSKPSSASSASLEKRMKWWSQSITQRFRLSRDRKVAKS 359
QY 360 LAVIVSIFGLCWAPYTLMLIRAAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHHSF 419
DB 360 LAIIVSIFGLCWAPYTLMLIRAAACHGHCVPDYWYETSFLLWANSVNPVLYPLCHYSF 419
QY 420 RRAFTKLLCPQKLTQPHSSLEHCWK 445
DB 420 RRAFTKLLCPQKLTQPHSSLEHCWK 445

RESULT 4
HH3R_RAT STANDARD; PRT; 445 AA.
AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Histamine H3 receptor (HH3R).
GN Name=Hrh3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;

[1]
SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Hypothalamus;
MEDLINE=20330707; PubMed=10869375;
Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Erlander M.G.;
"Cloning of rat histamine H3 receptor reveals distinct species
pharmacological profiles.";
J. Pharmacol. Exp. Ther. 293:771-778 (2000).
[2]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE=Striatum;
MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;
Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,
Stark H., Schunack W., Ganellin C.R., Schwartz J.-C., Arrang J.-M.;
"High constitutive activity of native H3 receptors regulates histamine
neurons in brain.";
Nature 408:860-864 (2000).
[3]
SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
Itadani H., Takimura T., Nakamura T., Ohta M.;
"Cloning of a novel G protein-coupled receptor.";
Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
[4]
TISSUE SPECIFICITY.
MEDLINE=99278519; PubMed=10347254;
Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
Huvar A., Jackson M.R., Erlander M.G.;
"Cloning and functional expression of the human histamine H3
receptor.";
Mol. Pharmacol. 55:1101-1107 (1999).
CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the
histamine signals in CNS and peripheral nervous system. Signals
through the inhibition of adenylyl cyclase and displays high
constitutive activity (spontaneous activity in the absence of
agonist).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Comment=Additional isoforms seem to exist;
Name=1; Synonyms=H3L;
IsoId=Q9QYN8-1; Sequence=Displayed;
Name=2; Synonyms=H3S;
IsoId=Q9QYN8-2; Sequence=VSP_001887;
Name=3;
IsoId=Q9QYN8-3; Sequence=VSP_001888;
Name=4;
IsoId=Q9QYN8-4; Sequence=VSP_001889;
CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain, most notably
throughout the thalamus, the ventromedial hypothalamus and the
caudate nucleus. Isoform 1 is largely predominant in all tissues.
CC -!- MISCELLANEOUS: Proxifen acts as a potent neutral antagonist while
thioperamide, ciproxifan and FUB465 act as potent inverse
agonists.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
```

DR	PRINTS; PR00237; GPCRHHODPSN.
DR	PRINTS; PR01471; HISTAMINEH3R.
DR	PROSITE; PS00237; G_PROTEIN RECF_F1_1; 1.
DR	PROSITE; PS00262; G_PROTEIN RECF_F1_2; 1.
KW	Alternative splicing; G-protein coupled receptor; Glycoprotein;
KW	Transmembrane.
FT	DOMAIN 1 39 Extracellular (Potential).
FT	TRANSMEM 40 60 Potential.
FT	DOMAIN 61 70 Cytoplasmic (Potential).
FT	TRANSMEM 71 91 Potential.
FT	DOMAIN 92 108 Extracellular (Potential).
FT	TRANSMEM 109 129 Potential.
FT	DOMAIN 130 156 Cytoplasmic (Potential).
FT	TRANSMEM 157 177 Potential.
FT	DOMAIN 178 196 Extracellular (Potential).
FT	TRANSMEM 197 217 Potential.
FT	DOMAIN 218 359 Cytoplasmic (Potential).
FT	TRANSMEM 360 380 Potential.
FT	DOMAIN 381 396 Extracellular (Potential).
FT	TRANSMEM 397 417 Potential.
FT	DOMAIN 418 445 Cytoplasmic (Potential).
FT	DOMAIN 20 23 Poly-Ala.
FT	CARBOHYD 11 11 N-linked (GlcNAc.. ) (Potential).
FT	VARSPLIC 274 305 Missing (in isoform 2).
FT	
FT	VARSPLIC 274 321 /FTid=VSP 001887.
FT	
FT	VARSPLIC 393 445 Missing (in isoform 3 and isoform 4).
FT	
FT	VARSPLIC 393 445 /FTid=VSP 001888.
FT	
FT	WVESFWLLWANSANVPVLPLCHVSFRRAFTKLCPOKLK
FT	VQPGSLQCWK -> CYERGLKEASILLPLLMWESGRWR
FT	RKHVELDPWMFNQRNCRGAWIGRGLPRPPPSVLQ
FT	LPAEPQLLPAPPEGLRWPCPACPVCTIRIWGWVMG
FT	(in isoform 4).
FT	/FTid=VSP 001889.
SEQ	SEQUENCE 445 AA; 48588 MW; 63DFEFC2I758FE5B CRC64;
Query Match 93.7%; Score 2213; DB 1; Length 445;	
Best Local Similarity 93.5%; Pred. NO. 4.3e-118;	
Matches 417; Conservative 9; Mismatches 18; Indels 2; Gaps 2	
Qy	1 MERAPPDGLNASGALGDAAAAGARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV 60
Dd	1 MERAPPDGLMASGTLAGEAAGAARGFSAAWTAVLAALMALLIVATVLGNALVMLAFV 60
Qy	61 ADSSLRTQNNEFLNLAIISDLFVGAFCLPLVYPYVLTGRWTFGRGLCKLWLVDYLCTS 120
Dd	61 ADSSLRTQNNEFLNLAIISDLFVGAFCLPLVYPYVLTGRWTFGRGLCKLWLVDYLCLS 120
Qy	121 SAFNVILISYDRFLSVTRAVSYRAQQGDTTRAVERKMLLVWVLAFLLYGPAILSWELSGG 180
Dd	121 SVFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVERKMLLVWVLAFLLYGPAILSWELSGG 180
Qy	181 SSIPEGHCYAEEFFNNWYELLITASTLEPTTFLSVTFNNLSYLNINQRTLRLDGAREAA 240
Dd	181 SSIPEGHCYAEEFFNNWYELLITASTLEPTTFLSVTFNNLSYLNINQRTLRLDGGRE-A 239
Qy	241 GPPEPPAQPSPPP~PPCCWGCKWGKGCEAMP LHRYGVGEEAAGVAEGEATLGCGGGGGS 299
Dd	240 GPPEPPDQPSPPPAPPSCWCWPKGHEAMP LHRYGVEAGPGVEAGEAALCGSGGGGA 299
Qy	300 VASPTSSSGSSSRGTERPRSRLKRSGSKPSASSASLEKRMKWYSQSFTORFRLSRDRKVAKS 359
Dd	300 AASFSSSGSSSRGTERPRSRLKRSGSKPSASSASLEKRMKWYSQSITQRFRLSRDKVKAKS 359
Qy	360 LAVTVSIFGLCWAPYTLLMIIRAACHGHCVDDPYTWYETSFLLWANSANVPYLPLCHHSF 419
Dd	360 LAITVISIFGLCWAPYTLLMIIRAACHGRCIPDYWYETSFLLWANSANVPYLPLCHYSF 419
Qy	420 RRAFTKLLCPOKLKIQPHSSLEHCWK 445
Dd	420 RRATKKLLCPOKLKIQPHGLEQCWK 445
RESULT 5	

## RESULT 5

```
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARGPLIC 276 305 Missing (in isoform Short).
FT /FTIC=VSP 001880.
SQ SEQUENCE 445 AA; 48734 MW; BA206A3887189A0 CRC64;

Query Match
Best Local Similarity 92.3%; Score 2179; DB 1; Length 445;
Matches 415; Conservative 10; Mismatches 18; Indels 4; Gaps 3;

QY 1 MERAPPDGLNAGSAGALAGD-AAAAGGARGFSAWTAVALAALLMALLIVATVIGNALVMLAF 59
DQ 1 MERAPPDGLNAGSAGALAGD-AAAAGGARGFSAWTAVALAALLMALLIVATVIGNALVMLAF 60
QY 60 VADSSLRTQNNFFLNLAISDFLVGAFICPLVVPVVLTCGRWTFGRGLCKMLVVDVLLCT 119
DQ 61 VADSSLRTQNNFFLNLAISDFLVGAFICPLVVPVVLTCGRWTFGRGLCKMLVVDVLLCT 120
QY 120 SSANFNLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSSG 179
DQ 121 SSVFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSSG 180
QY 180 GSSIEGHCHYABFFNYWYFLITASTLEFPTPLSVTFNLSIYINIQRTLRRLDGAEEA 239
DQ 181 GSSIEGHCHYABFFNYWYFLITASTLEFPTPLSVTFNLSIYINIQRTLRRLDGAEEA 240
QY 240 AGPEPPPEAQPSP-PPPGCWGCKGHEAMPLHRYGVGEAAVCAEAGEATLGGGGGGG 298
DQ 241 AGPDPLPQAQSP-PPPGCWGCKGHEAMPLHRYGVGEAGPAGAEAGEAAL--GGGGG 298
QY 299 SVAPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFTQRFRLSRDRKVKAK 358
DQ 299 AAAPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFTQRFRLSRDRKVKAK 358
QY 359 SLAVISIFGLCWAPYTLMIIRAACHGCHVDPYVYETSFLLWANSVNPVLYPLCHHS 418
DQ 359 SLAVISIFGLCWAPYTLMIIRAACHGCHVDPYVYETSFLLWANSVNPVLYPLCHYS 418
QY 419 FRRAFTKLLCPQKIKIOPHSSLEHCWK 445
DQ 419 FRRAFTKLLCPQKIKIOPHSSLEHCWK 445

RESULT 6
Q8WXZ9 PRELIMINARY; PRT; 365 AA.
ID Q8WXZ9
AC Q8WXZ9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 2.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF321911; AAL71912.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSIN.

PRINTS; PR01471; HISTAMINEH3R.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 365 AA; 40609 MW; D78B3204246CB35 CRC64;

Query Match
Best Local Similarity 82.0%; Score 1919; DB 2; Length 365;
Matches 365; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MERAPPDGLNAGSAGALAGD-AAAAGGARGFSAWTAVALAALLMALLIVATVIGNALVMLAF 60
DQ 1 MERAPPDGLNAGSAGALAGD-AAAAGGARGFSAWTAVALAALLMALLIVATVIGNALVMLAF 60
QY 61 ADSSLRTQNNFFLNLAISDFLVGAFICPLVVPVVLTCGRWTFGRGLCKMLVVDVLLCT 120
DQ 61 ADSSLRTQNNFFLNLAISDFLVGAFICPLVVPVVLTCGRWTFGRGLCKMLVVDVLLCT 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSSG 180
DQ 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSSG 180
QY 181 SSIPEGHCYABFFNYWYFLITASTLEFPTPLSVTFNLSIYINIQRTLRRLDGAEEA 240
DQ 181 SSIPEGHCYABFFNYWYFLITASTLEFPTPLSVTFNLSIYINIQRTLRRLDGAEEA 240
QY 241 GPEPPPEAQPSP-PPPGCWGCKGHEAMPLHRYGVGEAAVCAEAGEATLGGGGGGG 300
DQ 241 GPEPPPEAQPSP-PPPGCWGCKGHEAMPLHRYGVGEAAVCAEAGEATLGGGGGGG 300
QY 301 ASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFTQRFRLSRDRKVKAKSL 360
DQ 274 -----RKVAKSL 280
QY 361 AVISIFGLCWAPYTLMIIRAACHGCHVDPYVYETSFLLWANSVNPVLYPLCHHSFR 420
DQ 281 AVISIFGLCWAPYTLMIIRAACHGCHVDPYVYETSFLLWANSVNPVLYPLCHHSFR 340
QY 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445
DQ 341 RAFTKLLCPQKIKIOPHSSLEHCWK 365

RESULT 7
Q8WXZ9 PRELIMINARY; PRT; 373 AA.
ID Q8WXZ9
AC Q8WXZ9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 4.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF321913; AAL71914.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR Pfam; PF00001; 7tm_1; 1.
```

```

DR PRINTS; PRO0237; GPCRHHODOPSN.
DR PRINTS; PRO1471; HISTAMINEH3R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 373 AA; 41570 MW; FA59DFC53AF4DE9 CRC64;

Query Match      81.3%; Score 1919; DB 2; Length 373;
Best Local Similarity 82.0%; Pred. No. 1.8e-101;
Matches 365; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MERAPPDGLNAGSALAGDAAAGARGFSAWTAVALAALMALLIVATVIGNALVMLAFV 60
DB 1 MERAPPDGLNAGSALAGDAAAGARGFSAWTAVALAALMALLIVATVIGNALVMLAFV 60
QY 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
DB 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNYFLITASTLEFFTPFLSVTFNNLSIYLNITQRTRRLDGDAREAA 240
DB 181 SSIPGHCYAEFFYNYFLITASTLEFFTPFLSVTFNNLSIYLNITQRTRRLDGDAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLH----- 273
QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMSQSFTQRFRLSDRKVAKSL 360
DB 274 -----RKVAKSL 280
QY 361 AVISIFGLCWAPYTLMLIRAAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR 420
DB 281 AVISIFGLCWAPYTLMLIRAAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR 340
QY 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445
DB 341 RAFTKLLCPQKLIKIOPHSSLEHCWK 365

RESULT 8
Q8WY00 PRELIMINARY; PRT; 301 AA.
AC Q8WY00;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 3.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W.; Burstein E.S.; Nash N.R.; Brann M.R.;
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF321912; AAL71913.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

DR PRINTS; PRO0237; GPCRHHODOPSN.
DR PRINTS; PRO1471; HISTAMINEH3R.
DR PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; 1.
DR PROSITE; PS00262; G PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 301 AA; 33280 MW; EE740A2E0AB93CC9 CRC64;

Query Match      64.4%; Score 1521; DB 2; Length 301;
Best Local Similarity 67.6%; Pred. No. 6e-79;
Matches 301; Conservative 0; Mismatches 0; Indels 144; Gaps 1;

QY 1 MERAPPDGLNAGSALAGDAAAGARGFSAWTAVALAALMALLIVATVIGNALVMLAFV 60
DB 1 MERAPPDGLNAGSALAGDAAAGARGFSAWTAVALAALMALLIVATVIGNALVMLAFV 60
QY 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
DB 61 ADSSLRTQNNFLLNLAISDFLVGAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
QY 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
DB 121 SAFNVLISYDRFLSVTRAVSYRAQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCYAEFFYNYFLITASTLEFFTPFLSVTFNNLSIYLNITQRTRRLDGDAREAA 240
DB 181 SSIPGHCYAEFFYNYFLITASTLEFFTPFLSVTFNNLSIYLNITQRTRRLDGDAREAA 240
QY 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV 300
DB 241 GPEPPEAQSPPPPPGCGWKQKGHEAMPL----- 272
QY 301 ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMSQSFTQRFRLSDRKVAKSL 360
DB 273 ----- 272
QY 361 AVISIFGLCWAPYTLMLIRAAACHGCVDPYWTYSFWLLWANSVNPVLPCHHSFR 420
DB 273 -----HSFR 276
QY 421 RAFTKLLCPQKLIKIOPHSSLEHCWK 445
DB 277 RAFTKLLCPQKLIKIOPHSSLEHCWK 301

RESULT 9
Q8NI49 PRELIMINARY; PRT; 309 AA.
AC Q8NI49;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Histamine H3 receptor isoform 6.
GN Name=HRH3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Hippocampus;
RA Wellendorph P.; Goodman M.W.; Burstein E.S.; Nash N.R.; Brann M.R.;
RA Weiner D.M.;
RT "Molecular Cloning and Characterization of Functionally Distinct
RT Isoforms of the Human Histamine H3 Receptor.";
RL Neuropharmacology 0:0-0(2002).
CC -|- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -|- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF346904; AAM43829.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004969; F:histamine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.

```



DR GO: 0007186; P-G-protein coupled receptor protein signalin. . . ; IEA.  
DR InterPro: IPR000276; GPCR\_Rhodopsn.  
DR InterPro: IPR003980; H3\_receptor.  
DR Pfam: PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODOPSN.  
DR PRINTS; PR01471; HISTAMINEH3R.  
DR PROSITE; PS00237; G PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS00262; G PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 309 AA; 34242 MW; B7496F7DD2A206B CRC64;

Query Match 64.4%; Score 1521; DB 2; Length 309;  
Best Local Similarity 67.6%; Pred. No. 6.2e-79;  
Matches 301; Conservative 0; Mismatches 0; Indels 144; Gaps 1;

QY 1 MERAPDPGLNAGSALAGDAAAGARGFSAWTAVALAALLMALLIVATVGLNALVMAFV 60  
DB 1 MERAPDPGLNAGSALAGDAAAGARGFSAWTAVALAALLMALLIVATVGLNALVMAFV 60  
QY 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLVYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120  
DB 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLVYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120  
QY 121 SAFNVLISYDRFLSVTRAVSRAOQDTRRAVRKMLLVWVLAFLLYGPAILSWELSGG 180  
DB 121 SAFNVLISYDRFLSVTRAVSRAOQDTRRAVRKMLLVWVLAFLLYGPAILSWELSGG 180  
QY 181 SSIPGHCVAEFPYNYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCVAEFPYNYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
QY 241 GPEPPEAQPSPPPGCGWCKGHEAMPVLRHYGVGEAAGATLGGGGGGGSV 300  
DB 241 GPEPPEAQPSPPPGCGWCKGHEAMPVLRHYGVGEAAGATLGGGGGGGSV 300  
QY 301 ASPTSSSGSSRGTERPSLRKSGKPSASSASLEKRMKMWVSQFTQRFRLSRDKRVAKSL 360  
DB 273 ----- 272  
QY 361 AVIVSIFGLCWAPYTLMLIIRAACHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFR 420  
DB 273 -----HSFR 276  
QY 421 RAFTKLLCPQKLIQPHSSLEHCWK 445  
DB 277 RAFTKLLCPQKLIQPHSSLEHCWK 301

RESULT 10  
Q8K116 ID Q8K116 PRELIMINARY; PRT; 247 AA.  
AC Q8K116; DB 2; Length 247;  
DT 01-OCT-2002 (Tremblrel. 22, Created)  
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Hrh3 protein (Fragment).  
GN Name=Hrh3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zordan B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore S.I., Wang J., Hong L.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;  
RA Strausberg R.;  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC028947; AAH28947.1; -;  
DR MGI; MGI:2139279; Hrh3.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm1; 1.  
DR PRINTS; PR00237; GPCRHHODOPSN.  
DR PRINTS; PR01471; HISTAMINEH3R.  
DR PROSITE; PS00262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
FT NON\_TER 1  
SQ SEQUENCE 247 AA; 26937 MW; D0154BD9995A01B1 CRC64;

Query Match 51.8%; Score 1223; DB 2; Length 247;  
Best Local Similarity 91.5%; Pred. No. 4.2e-62;  
Matches 227; Conservative 6; Mismatches 13; Indels 2; Gaps 2;

QY 199 LITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAAAGPEPPEAQPSPPP 257  
DB 1 LITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAAAGPEPPEAQPSPPP 59  
QY 258 CWGQWQKCHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFRRAFTKLLCPQKLIQPH 317  
DB 60 CWGQWQKCHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFRRAFTKLLCPQKLIQPH 119  
QY 318 RSLKRGSKPSASSASLEKRMKMWVSQFTQRFRLSRDKRVAKSLAVIVSIFGLCWAPYTL 377  
DB 120 RSLKRGSKPSASSASLEKRMKMWVSQFTQRFRLSRDKRVAKSLAVIVSIFGLCWAPYTL 179  
QY 378 MIIRAACHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFRRAFTKLLCPQKLIQPH 437  
DB 180 MIIRAACHGCHVDPYVWYTSFWLLWANSVNPVLYPLCHHFRRAFTKLLCPQKLIQPH 239  
QY - 438 SLEHCWK 445  
DB 240 GSLEHCWK 247

RESULT 11  
Q8ZM33 ID Q8ZM33 PRELIMINARY; PRT; 473 AA.  
AC Q8ZM33;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE SI1b234G2.4 (Novel protein similar to human histamine receptor H3 (HRH3)).  
GN Name=si:rp71-34g2.4; Synonyms=SI:b234G2.4;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Tracey A.;  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AL928906; CAE49238.1; -.  
DR ZFIN; ZDB-GENE-040724-204; si:rp71-34g2.4.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004969; F:histamine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1\_receptor.  
DR PRINTS; PR00237; GPCRRHODOPSIN.  
DR PRINTS; PR01471; HISTAMINEH3R.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 473 AA; 53506 MW; 032FC7C27D8C65E7 CRC64;

Query Match 50.2%; Score 1186; DB 2; Length 473;  
Best Local Similarity 54.2%; Pred. No. 9.5e-60;  
Matches 240; Conservative 51; Mismatches 86; Indels 66; Gaps 8;  
QY 29 FSAWTAVALMALMALLIVATVGLNVALMFLAVDSSLRATONNFFLLNLAISDFLVGACFI 88  
DB 59 FSPSTSIETLVMLTLLVFATVGLNALVILAFVVEKSLRTQGNFFFLNLAIAADFLVGGFCI 118  
QY 89 PLYVPVLTGTWTFGRGLCKLWLVVDYLLCTSSAFNVLISVDRLSVTRAVSVRAQOQD 148  
DB 119 PVYIPVLTGTWTFGRGLCKLWLVVDYLLCTSSAFNVLISVDRLSVTRAVSVRAQOQD 178  
QY 149 TRRAVRKMLLVVLAFLYGPAILSWEYLSGSSSIPEGHCVAEFFYNWFLITASTLEFF 208  
DB 179 TKDAVLKMLCVLAFLYGPAILSWEYLSGSSSIPEGHCVAEFFYNWFLITASTLEFF 238  
QY 209 TPFLSVTFNLSIYLNIOQRTRLDGAREAGPPEPPPEAOPS-----PPPPPCW 259  
DB 239 TPFLSVTFNLSIYLNIRNCAMR-----EEOPTYVRLRSFVKMP----- 278  
QY 260 GCWQKHGEAM-----PLHRYGVGEAAVGAAGEATLGGGGGGSVASPTSSSSSSRG 313  
DB 279 ----LGAGDVQVRFVRPVEESRVADLASRCCRL-----ASTAKVSAAEFGNGRQ 326  
QY 314 TERPRSLKRGSKP-----SASSASL-----EKRMKMSQSFTQRFRLSRDRK 355  
DB 327 SKRRDSTLADLPPLQVEERILLAASEAQHYVDHSAGPHRHPDMA-SLANRFLSRDRK 385  
QY 356 VAKSLAVIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWYTSFWLLWANSVNPVLYPLC 415  
DB 386 VAKSLAVIVCVFGLCWAPYTLMIIRAACHGCHVDPDYWYTSFWLLWANSVNPVLYPLC 445  
QY 416 HHSFRAFTKLLCPQKLIQPHS 438  
DB 446 HSSFKRAFSKLLCPSTKIQQON 468

RESULT 12  
Q8NCH4 PRELIMINARY; PRT; 210 AA.  
ID Q8NCH4  
AC Q8NCH4; 210 AA.  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Hypothetical protein FLJ90249.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Itoigai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,  
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,  
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK074730; BAC11167.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004969; F:histamine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR InterPro; IPR003980; H3\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1\_receptor.  
DR PRINTS; PR00237; GPCRRHODOPSIN.  
DR PRINTS; PR01471; HISTAMINEH3R.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
KW Receptor.  
SQ SEQUENCE 210 AA; 24046 MW; 952F3FFD60077CAD CRC64;  
Query Match 48.2%; Score 1137; DB 2; Length 210;  
Best Local Similarity 72.4%; Pred. No. 2.8e-57;  
Matches 210; Conservative 0; Mismatches 0; Indels 80; Gaps 1;  
QY 156 MLLVWVLAFLYGPAILSWEYLSGSSSIPEGHCVAEFFYNWFLITASTLEFFPFLSVT 215  
DB 1 MLLVWVLAFLYGPAILSWEYLSGSSSIPEGHCVAEFFYNWFLITASTLEFFPFLSVT 60  
QY 216 FPNLSIYLNIOQRTRLDGAREAGPPEPPPEAOPSPPPPPCWQKQHGAEAMPLHRY 275  
DB 61 FPNLSIYLNIOQRTRLDGAREAGPPEPPPEAOPSPPPPPCWQKQHGAEAMPLH-- 118  
QY 276 GVGEAAVGAAGEATLGGGGGGSVASPTSSSSSSRGTERRSLKRGSKPSASSASLEK 335  
DB 119 ----- 118  
QY 336 RMKMSQSFTQRFRLSRDRKVAKSLAVIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWE 395  
DB 119 -----RKVAKSLAVIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWE 160  
QY 396 TSFWLLWANSVNPVLYPLCHHSFRAFTKLLCPQKLIQPHSSSLEHCWK 445  
DB 161 TSFWLLWANSVNPVLYPLCHHSFRAFTKLLCPQKLIQPHSSSLEHCWK 210  
RESULT 13  
Q8N150 PRELIMINARY; PRT; 200 AA.  
ID Q8N150  
AC Q8N150;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Histamine H3 receptor isoform 5.  
GN Name=HRH3;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Hippocampus;  
RA Wellendorph P., Goodman M.W., Burstein E.S., Nash N.R., Brann M.R.,  
RA Weiner D.M.;  
RT Molecular Cloning and Characterization of Functionally Distinct  
RT Isoforms of the Human Histamine H3 Receptor.;  
EL Neuropharmacology 0:0-0(2002).  
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -I- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF346903; AAM43828.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004969; F:histamine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; IEA.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.

DR InterPro; IPR003980; H3 receptor.  
DR Pfam; PF00001; 7tm 1; 1-  
DR PRINTS; PRO0237; GPCRHOODPSN.  
DR PRINTS; PRO1471; HISTAMINEHR3.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 200 AA; 21612 MW; 2038D14BC186D1EA CRC64;  
  
Query Match 36.4%; Score 860; DB 2; Length 200;  
Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MERAPPDGLNAGSALAGDAAGAGSAAWTAVALAALLVATVGLNGLVLAFAV 60  
DB 1 MERAPPDGLNAGSALAGDAAGAGSAAWTAVALAALLVATVGLNGLVLAFAV 60  
  
QY 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120  
DB 61 ADSSLRQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120  
  
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPA 170  
DB 121 SAFNVLISYDRFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPA 170  
  
RESULT 14  
Q865E3 PRELIMINARY; PRT; 147 AA.  
ID Q865E3  
AC Q865E3  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-WAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Histamine receptor H3 (fragment).  
GN Name=HRH3;  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI\_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Witte D.G., Ebershade T.A., Hancock A.A., Yao B.B.;  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
DR EMBL; AY231165; AAO63755.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004969; F:histamine receptor activity; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR InterPro; IPR0007186; P:G-protein coupled receptor protein signal. . .; IEA.  
DR InterPro; IPR000276; GPCR Rhodpsn.  
DR Pfam; PF00001; 7tm 1; 1-  
DR PRINTS; PRO0237; GPCRHOODPSN.  
DR PRINTS; PRO1471; HISTAMINEHR3.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
FT NON\_TER 1  
FT NON\_TER 147  
SQ SEQUENCE 147 AA; 16900 MW; 67F6A741B518B54E CRC64;  
  
Query Match 31.9%; Score 754; DB 2; Length 147;  
Best Local Similarity 95.9%; Pred. No. 1.2e-35;  
Matches 141; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
QY 72 FLNLNLAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISVD 131  
DB 1 FLNLNLAISDFLVGAFICPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISVD 60  
  
QY 132 RFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPAISWELSGGSSIPGHCYAE 191  
DB 132 RFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPAISWELSGGSSIPGHCYAE 191

DB 61 RFLSVTRAVSYRAOQDTRRAVRKMLLVWVLAFLLYGPAISWELSGGSSIPGHCYAE 120  
QY 192 FFYNNYFLITASTLEFFTPFLSVTFEN 218  
DB 121 FFYNNYFLITASTLEFFTPFLSVTFEN 147  
  
RESULT 15  
HH4R\_HUMAN  
ID HH4R\_HUMAN STANDARD; PRT; 390 AA.  
AC Q9H3N8; Q9CZQ0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105)  
DE (GPCR105) (SP9144) (AXOR35).  
GN Name=HRH4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=205338417; PubMed=10973974; DOI=10.1074/jbc.M006480200;  
ODA T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.-I.;  
RT "Molecular cloning and characterization of a novel type of histamine  
receptor preferentially expressed in leukocytes";  
RL J. Biol. Chem. 275:36781-36786(2000).  
RN [2]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Leukocyte;  
RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;  
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;  
RT "Molecular cloning and characterization of a new human histamine  
receptor, HH4R";  
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Jones P.G., Wu S., Betty M.;  
RT "Cloning of a novel histamine receptor";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Bone marrow;  
RX PubMed=11179434;  
RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J.,  
Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.;  
RT "Cloning and pharmacological characterization of a fourth histamine  
receptor (H4) expressed in bone marrow";  
RL Mol. Pharmacol. 59:420-426(2001).  
RN [5]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Eosinophil;  
RX MEDLINE=21104636; PubMed=11181941;  
RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A.,  
Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N.,  
Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M.,  
Monsma F.J. Jr.;  
RT "Cloning and characterization of a novel human histamine receptor";  
RL J. Pharmacol. Exp. Ther. 296:1058-1066(2001).  
RN [6]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21106320; PubMed=11179436;  
RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J.,  
Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L.,  
Sarau H.M., Ames R.S., Davenport C.M., Hieble P., Wilson S.,  
Bergsma D.J., Fitzgerald L.R.;  
RT "Cloning, expression, and pharmacological characterization of a novel  
human histamine receptor";  
RL Mol. Pharmacol. 59:434-441(2001).  
RN [7]  
RP SEQUENCE FROM N.A.  
RA O'Reilly M.A.;



**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 2, 2005, 05:14:06 ; Search time 445.596 Seconds  
(without alignments)  
9911.021 Million cell updates/sec

Title: US-10-727-021-5  
Perfect score: 2699  
Sequence: 1 ccacgcgtccgcgggtgca.....aaaaaaaaaaaaaaaaaaaaa 2699

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2699	100.0	2699	3	US-09-167-354-5
2	2699	100.0	2699	3	US-09-642-855-8
3	2699	100.0	2699	3	US-09-642-514-5
4	2635.2	97.6	2689	2	US-08-985-090-1
5	2635.2	97.6	2689	3	US-09-165-543-1
6	2633.6	97.6	2665	4	US-09-949-016-5059
7	1947.8	72.2	9293	4	US-09-949-016-16801
8	1590.2	58.9	1893	4	US-09-891-053-13
9	1384.8	51.3	3244	3	US-09-165-543-4
10	1360.4	50.4	2050	4	US-09-891-053-21
11	1335	49.5	1335	3	US-09-167-354-6
12	1335	49.5	1335	3	US-09-642-855-6
13	1335	49.5	1335	3	US-09-642-514-6
14	1331.8	49.3	1335	2	US-08-985-090-3
15	1331.8	49.3	1335	3	US-09-165-543-3
16	1208	44.8	2700	4	US-09-891-053-5
17	1201.8	44.5	1953	4	US-09-891-053-26
18	1072.2	39.7	1338	3	US-09-165-543-6
19	1032.6	38.3	2218	2	US-08-985-090-4
20	1032.6	38.3	2218	3	US-09-165-543-31
21	899.2	33.3	1239	4	US-09-891-053-2
22	852.2	31.6	1086	2	US-08-985-090-6
23	852.2	31.6	1086	3	US-09-165-543-33
24	750.8	27.8	1056	3	US-09-524-162-1
25	600.6	22.3	601	4	US-09-949-016-177027
26	525.4	19.5	1350	4	US-09-891-053-11
27	375	13.9	375	3	US-09-167-354-8

c

28	375	13.9	375	3	US-09-642-855-8	Sequence 8, Appli
29	375	13.9	375	3	US-09-642-514-8	Sequence 8, Appli
30	177.4	6.6	3604	4	US-09-016-434-1180	Sequence 1180, Ap
31	175.2	6.5	1956	1	US-08-313-553-6	Sequence 6, Appli
32	175.2	6.5	1956	3	US-08-767-993-6	Sequence 6, Appli
33	175	6.5	2595	4	US-09-016-434-1178	Sequence 1178, Ap
34	173.6	6.4	1440	4	US-09-826-509-518	Sequence 518, App
35	173.4	6.4	448	4	US-09-891-053-12	Sequence 12, Appl
36	173.2	6.4	1422	4	US-09-826-509-512	Sequence 512, App
37	172.4	6.4	1581	1	US-08-313-553-8	Sequence 8, Appli
38	172.4	6.4	1581	3	US-08-767-993-8	Sequence 8, Appli
39	171.6	6.4	1386	4	US-09-016-434-1339	Sequence 1339, Ap
40	162.6	6.0	1382	4	US-09-016-434-1256	Sequence 1256, Ap
41	155.6	5.8	1599	4	US-09-826-509-520	Sequence 520, App
42	155.6	5.8	2261	4	US-09-016-434-1176	Sequence 1176, Ap
43	143.2	5.3	1845	4	US-09-614-034-188	Sequence 188, App
44	138.6	5.1	4401	4	US-09-614-034-192	Sequence 192, App
45	131	4.9	1344	4	US-09-825-923-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-167-354-5  
; Sequence 5, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-167-354-5

Query Match	100.0%;	Score 2699;	DB 3;	Length 2699;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2699;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	CCACGGGTCCGCGGGTGCACGGTTCGCACCGGACGGGCTCAGGCTCCGGCTCCTCTCCC	60	
Db	1	CCACGGGTCCGCGGGTGCACGGTTCGCACCGGACGGGCTCAGGCTCCGGCTCCTCTCCC	60	
QY	61	GCTGCACGACGCGGTGCGGGCCCTGCGGCTTCGATCCGCGCCCGGGCCCTCTCGGCA	120	
Db	61	GCTGCACGACGCGGTGCGGGCCCTGCGGCTTCGATCCGCGCCCGGGCCCTCTCGGCA	120	
QY	121	CCGCTGCTCTGGCCCCGGCCCCGGCGGACCATGCGCTGGGGCGCCCCCAGAGGGAA	180	
Db	121	CCGCTGCTCTGGCCCCGGCCCCGGCGGACCATGCGCTGGGGCGCCCCCAGAGGGAA	180	
QY	181	ACCGACCCGGCCAAAGGGCCCGCAAGACGAGGCTCCGGGCGGGGCGCCCTCTCCGGCCG	240	
Db	181	ACCGACCCGGCCAAAGGGCCCGCAAGACGAGGCTCCGGGCGGGGCGCCCTCTCCGGCCG	240	
QY	241	CCGAGTCTTCGGCGGGCGCCCTGCCCCCGCTCCCGAGCCGCTGAGCCTCGGGGGCCAT	300	
Db	241	CCGAGTCTTCGGCGGGCGCCCTGCCCCCGCTCCCGAGCCGCTGAGCCTCGGGGGCCAT	300	
QY	301	GGAGCGCGCCCGCCGACGGGGCGCTGAACGCTTCGGGGCGCGTGGCGGGCGATGCGGC	360	

Db 301 GGAGCGCGCGCGCGCGCGCGCGCTGAA CGCTTCGGGGGGCGCTGGCGGGCGATGCGGC 360  
QY 361 GCGCGGGCGGGCGGGCGGGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCGCGCGCTCAT 420  
Db 361 GCGCGGGCGGGCGGGCGGGCTTCTCGGCAGCCTGGACCGCGGTGCTGGCGCGCGCTCAT 420  
QY 421 GCGCGTGTCTCATGCTGGCGCGCGCGGTGCTGGCAACCGCTGGTCACTGCTGCGCTTCTGTCG 480  
Db 421 GCGCGTGTCTCATGCTGGCGCGCGGTGCTGGCAACCGCTGGTCACTGCTGCGCTTCTGTCG 480  
QY 481 CGACTCGAGCCTCCGACCCAGCAAACTTCTTCGTCTCAACCTCGGCATCTCCGACTT 540  
Db 481 CGACTCGAGCCTCCGACCCAGCAAACTTCTTCGTCTCAACCTCGGCATCTCCGACTT 540  
QY 541 CTTGTCGGCGCTTCTGATCCCATCTGATATGATACCTACGTGCTGACAGGCGCGTGGAC 600  
Db 541 CTTGTCGGCGCTTCTGATCCCATCTGATATGATACCTACGTGCTGACAGGCGCGTGGAC 600  
QY 601 CTTGCGCGGGGCGCTTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACCTCTCTC 660  
Db 601 CTTGCGCGGGGCGCTTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGCACCTCTCTC 660  
QY 661 TGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGTCAACCGAGCGGTCTC 720  
Db 661 TGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGTCAACCGAGCGGTCTC 720  
QY 721 ATACCGGGCCAGAGAGGTGACACGGCGGGCAGTGGGAAAGATGCTGCTGGTGTGGGT 780  
Db 721 ATACCGGGCCAGAGAGGTGACACGGCGGGCAGTGGGAAAGATGCTGCTGGTGTGGGT 780  
QY 781 GCTGGCGCTTCTGCTGTACGGACAGCCATCTGAGCTGGGAGTACCTGCTCGGGGGCGAG 840  
Db 781 GCTGGCGCTTCTGCTGTACGGACAGCCATCTGAGCTGGGAGTACCTGCTCGGGGGCGAG 840  
QY 841 CTTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTACAACTGCTACTTCTCTCATCAC 900  
Db 841 CTTCCATCCCGAGGGCCACTGCTATGCGGAGTCTTCTACAACTGCTACTTCTCTCATCAC 900  
QY 901 GGCCTTCCACCTTGGAGTTCTTTAGCGCTTCTCAGCGTCACTTCTTTAACTCAGCAT 960  
Db 901 GGCCTTCCACCTTGGAGTTCTTTAGCGCTTCTCAGCGTCACTTCTTTAACTCAGCAT 960  
QY 961 CTTACCTGAACATCCAGAGCGCACCGCGCTCGGCTGGATGGGCTCGAGAGCGAGCGG 1020  
Db 961 CTTACCTGAACATCCAGAGCGCACCGCGCTCGGCTGGATGGGCTCGAGAGCGAGCGG 1020  
QY 1021 CCCCAGCGCCCTCCCGAGCGCCAGCCCTCAACACCCCGCCCTGCTGCTGGGGCTG 1080  
Db 1021 CCCCAGCGCCCTCCCGAGCGCCAGCCCTCAACACCCCGCCCTGCTGCTGGGGCTG 1080  
QY 1081 CTGGCAGAAAGGGCACCGGGAGGCCCATGCGCTGCACAGGTATGGGGTGGGTGAGCGCGC 1140  
Db 1081 CTGGCAGAAAGGGCACCGGGAGGCCCATGCGCTGCACAGGTATGGGGTGGGTGAGCGCGC 1140  
QY 1141 CGTAGGCGCTGAGCGCGGGGAGCGGACCTCGGGGGTGGCGGTGGGGCGGCTCGTGGC 1200  
Db 1141 CGTAGGCGCTGAGCGCGGGGAGCGGACCTCGGGGGTGGCGGTGGGGCGGCTCGTGGC 1200  
QY 1201 TTTCAACCCACTCCAGCTCCGCGAGCTTCTCGAGGGGCACTGAGAGCGCCGCTCACTCAA 1260  
Db 1201 TTTCAACCCACTCCAGCTCCGCGAGCTTCTCGAGGGGCACTGAGAGCGCCGCTCACTCAA 1260  
QY 1261 GAGGGGCTCCAGCGCTCGCGGTCTCGCGCTCGCTGGGAGAGCGCATGAAGATGGTGTG 1320  
Db 1261 GAGGGGCTCCAGCGCTCGCGGTCTCGCGCTCGCTGGGAGAGCGCATGAAGATGGTGTG 1320  
QY 1321 CCAGAGCTTCCAGAGCTTTTGGGTGCTCGGGACAGAAAGTGGCCAACTCCGTGGC 1380  
Db 1321 CCAGAGCTTCCAGAGCTTTTGGGTGCTCGGGACAGAAAGTGGCCAACTCCGTGGC 1380  
QY 1381 CGTCACTGTGAGCATCTTTGGGTGCTCGTGGGGCCCATACAGCTGCTGATCATCCG 1440  
Db 1381 CGTCACTGTGAGCATCTTTGGGTGCTCGTGGGGCCCATACAGCTGCTGATCATCCG 1440

QY 1441 GGCGCGCTGCCATGGCCACTGGGTCCCTGACTACTGGTACGAAACCTCTTCTTGCTCT 1500  
Db 1441 GGCGCGCTGCCATGGCCACTGGGTCCCTGACTACTGGTACGAAACCTCTTCTTGCTCT 1500  
QY 1501 GTGGGCCAACTCGGCTGTCAAACCTGTCTTACCTCTGTGSCCACCACAGCTTCCGCG 1560  
Db 1501 GTGGGCCAACTCGGCTGTCAAACCTGTCTTACCTCTGTGSCCACCACAGCTTCCGCG 1560  
QY 1561 GGCCTTCAACAGGTGCTCTGCCCCCAGAGCTCAAAATCAGGCCCAACAGTCTCCTGGA 1620  
Db 1561 GGCCTTCAACAGGTGCTCTGCCCCCAGAGCTCAAAATCAGGCCCAACAGTCTCCTGGA 1620  
QY 1621 GCATGCTGGAAGTGAAGTGGGCCCAACAGAGCTCCCTCAGCAGCGCTCTCTCAGCCAG 1680  
Db 1621 GCATGCTGGAAGTGAAGTGGGCCCAACAGAGCTCCCTCAGCAGCGCTCTCTCAGCCAG 1680  
QY 1681 GTCTCTGGGCGATCTGGGCCCTGCTGCCCCCTACCGGCTCGTTCCCCAGGGGTGAGGCC 1740  
Db 1681 GTCTCTGGGCGATCTGGGCCCTGCTGCCCCCTACCGGCTCGTTCCCCAGGGGTGAGGCC 1740  
QY 1741 GCGCGTGTCTGTGGCCCTCTCTTAATGCCACGCGAGCCACCTGCTGCATGAGAGCGCCTTC 1800  
Db 1741 GCGCGTGTCTGTGGCCCTCTCTTAATGCCACGCGAGCCACCTGCTGCATGAGAGCGCCTTC 1800  
QY 1801 CTGGGTTGGCCAGAGGGCCCTCTCACTGGCTGGACTGGAGGCTGGGTGGCGCGCCCTGCC 1860  
Db 1801 CTGGGTTGGCCAGAGGGCCCTCTCACTGGCTGGACTGGAGGCTGGGTGGCGCGCCCTGCC 1860  
QY 1861 CCCATTTCTGGCTCCACCGGGGAGGACAGTCTGGAGGCTCCAGACATGTGCTGCCACCC 1920  
Db 1861 CCCATTTCTGGCTCCACCGGGGAGGACAGTCTGGAGGCTCCAGACATGTGCTGCCACCC 1920  
QY 1921 CTTGCTGTGCCCCACCTTTCGACGTTACTGTGTGGTGTCTTCCAAAGCAAGCACTGG 1980  
Db 1921 CTTGCTGTGCCCCACCTTTCGACGTTACTGTGTGGTGTCTTCCAAAGCAAGCACTGG 1980  
QY 1981 GTGTGCTCAGGCTTCTGCGCTTACGAGTTTTCCTCTCGACGTGCACACCTGCACACC 2040  
Db 1981 GTGTGCTCAGGCTTCTGCGCTTACGAGTTTTCCTCTCGACGTGCACACCTGCACACC 2040  
QY 2041 CTTGCACACACTGTCACACCGTCCCTCTCCCGGACAAAGCCAGGACACTGCTTTGCTG 2100  
Db 2041 CTTGCACACACTGTCACACCGTCCCTCTCCCGGACAAAGCCAGGACACTGCTTTGCTG 2100  
QY 2101 CTTCTGTCTCTTGATTAAGCTCAGGCTGCGCTTTCACCCCTCTTCCACCAACTCT 2160  
Db 2101 CTTCTGTCTCTTGATTAAGCTCAGGCTGCGCTTTCACCCCTCTTCCACCAACTCT 2160  
QY 2161 CTTGCCCCCAAAAGTGTCAAGGGGCCCTAGGAACTCGAAAGCTTCTGCTTTTCCA 2220  
Db 2161 CTTGCCCCCAAAAGTGTCAAGGGGCCCTAGGAACTCGAAAGCTTCTGCTTTTCCA 2220  
QY 2221 TTTCTGGGTGTTTCAAGAAAGATGAAGAAAGAAATGTGTGAATCTGATGTTCTGGG 2280  
Db 2221 TTTCTGGGTGTTTCAAGAAAGATGAAGAAAGAAATGTGTGAATCTGATGTTCTGGG 2280  
QY 2281 ATGTTTAATCAAGAGAGACAAATTTGTGAGAGCTCAGGGCTGATTTGGCAGGTGGG 2340  
Db 2281 ATGTTTAATCAAGAGAGACAAATTTGTGAGAGCTCAGGGCTGATTTGGCAGGTGGG 2340  
QY 2341 CTTCCACGCGCTCTCTCCCTCGCTAAGGCTTCCGCTGAGCTGCTGCTGCTGCTGCT 2400  
Db 2341 CTTCCACGCGCTCTCTCCCTCGCTAAGGCTTCCGCTGAGCTGCTGCTGCTGCTGCT 2400  
QY 2401 CACCCCGCTCTGGGCTCACACCGCTCTGGTGGCAAGCCCTGCCCGGCCACTCTGTTT 2460  
Db 2401 CACCCCGCTCTGGGCTCACACCGCTCTGGTGGCAAGCCCTGCCCGGCCACTCTGTTT 2460  
QY 2461 GCTCAACCCAGAGACTCTCTGGGGTGTGTTGGAGAGAGGGGGCCCGCTGGGCCCGAGGTCC 2520  
Db 2461 GCTCAACCCAGAGACTCTCTGGGGTGTGTTGGAGAGAGGGGGCCCGCTGGGCCCGAGGTCC 2520

QY 2521 CAAGGGTCCAGGGCGGTCCAGAGAGGTGCCCGGGCAGGGGCGCTTCGGCATGTGCT 2580  
Db 2521 CAAGGGTCCAGGGCGGTCCAGAGAGGTGCCCGGGCAGGGGCGCTTCGGCATGTGCT 2580  
QY 2581 GTGCACCGGTCCAGCGGCTCTGCATGCTCCTCTGCTGTCGCGTGGCTGCCCTGCA 2640  
Db 2581 GTGCACCGGTCCAGCGGCTCTGCATGCTCCTCTGCTGTCGCGTGGCTGCCCTGCA 2640  
QY 2641 AACCGTGAGGTCAATAAAGTGATTTTTTAAAAAAAAAAAAAAAAAAAAAA 2699  
Db 2641 AACCGTGAGGTCAATAAAGTGATTTTTTAAAAAAAAAAAAAAAAAAAAAA 2699

RESULT 2

US-09-642-855-5  
; Sequence 5, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Brlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: JWV  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; CURRENT FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; PRIOR FILING DATE: 1998-10-06  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-855-5

Query Match 100.0%; Score 2699; DB 3; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 2699; Conservative 0;  
QY 1 CCACGCGTCCGCGGCTGCACGGTCCGACCGGAGCGGCTCAGGCTCCGGCTCCTCTCC 60  
Db 1 CCACGCGTCCGCGGCTGCACGGTCCGACCGGAGCGGCTCAGGCTCCGGCTCCTCTCC 60  
QY 61 GTGCAGCAGCGCGCTGCGGCGCCCACTGGGCTCGGATCGGGCCCGGCGCCCTCGGCA 120  
Db 61 GTGCAGCAGCGCGCTGCGGCGCCCACTGGGCTCGGATCGGGCCCGGCGCCCTCGGCA 120  
QY 121 CGGCTGTCTGGCGCCCGGCGCCCGGCGGACCATGCGTGGGCGCGCCCGGCGGAA 180  
Db 121 CGGCTGTCTGGCGCCCGGCGCCCGGCGGACCATGCGTGGGCGCGCCCGGCGGAA 180  
QY 181 ACCGACCGGCAAGGGCGCCGAAAGACGAGGCTCCGGGCGGGGCGCCCTCCCGGCG 240  
Db 181 ACCGACCGGCAAGGGCGCCGAAAGACGAGGCTCCGGGCGGGGCGCCCTCCCGGCG 240  
QY 241 CCCAGCTCTGGCGCGGCGCTGCGCGCGCTCCCGAGCGCGTGGGCGGCGCAT 300  
Db 241 CCCAGCTCTGGCGCGGCGCTGCGCGCGCTCCCGAGCGCGTGGGCGGCGCAT 300  
QY 301 GGAGCGCGCGCGCGCGCGCGCTGAACTTTCGGGGCGCTGGGCGGCGATGCGGC 360  
Db 301 GGAGCGCGCGCGCGCGCGCGCTGAACTTTCGGGGCGCTGGGCGGCGATGCGGC 360  
QY 361 GGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGGCGTGGCGCGCTCAT 420  
Db 361 GGCGCGCGCGCGCGCGCGCTTCTCGGACGCTGGACCGGCGTGGCGCGCTCAT 420  
QY 421 GGCGCTGTCTAFCGTGGCCACGGTCTGGGCAACGCGTGTGTCATGCTCGCTTCGTGCG 480  
Db 421 GGCGCTGTCTAFCGTGGCCACGGTCTGGGCAACGCGTGTGTCATGCTCGCTTCGTGCG

Db 421 GGCGCTGTCTAFCGTGGCCACGGTCTGGGCAACGCGTGTGTCATGCTCGCTTCGTGCG 480  
QY 481 CGACTCGAGCCCTCCGCAACCCAGAAACAATTTCTTCTGTCTCAACCTCGCATCTCCGACTT 540  
Db 481 CGACTCGAGCCCTCCGCAACCCAGAAACAATTTCTTCTGTCTCAACCTCGCATCTCCGACTT 540  
QY 541 CTTGTCGGGCGCTTCTGCACTCCCACTGTATGTATGTAACCTACGTCGACAGGCGCTGGAC 600  
Db 541 CTTGTCGGGCGCTTCTGCACTCCCACTGTATGTATGTAACCTACGTCGTCGACAGGCGCTGGAC 600  
QY 601 CTTGSGCCGSGGCGCTTCTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
Db 601 CTTGSGCCGSGGCGCTTCTGCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660  
QY 661 TGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGTCGCTCACCGAGCGGTCTC 720  
Db 661 TGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGTCGCTCACCGAGCGGTCTC 720  
QY 721 ATACCGGCGCCAGCAGGCTGACACCGCGGGGCGAGTGGGGAAGATGCTGCTGTGTGGGT 780  
Db 721 ATACCGGCGCCAGCAGGCTGACACCGCGGGGCGAGTGGGGAAGATGCTGCTGTGTGGGT 780  
QY 781 GCTGSCCTTCTGCTGTACGACGACCATCTGAGCTGGGAGTACCTGTCCGSGGCGAG 840  
Db 781 GCTGSCCTTCTGCTGTACGACGACCATCTGAGCTGGGAGTACCTGTCCGSGGCGAG 840  
QY 841 CTCCATCCCGAGGCGCACTGTATGCGAGTCTTCTTACAACTGCTTCTTCTCATCATC 900  
Db 841 CTCCATCCCGAGGCGCACTGTATGCGAGTCTTCTTACAACTGCTTCTTCTCATCATC 900  
QY 901 GGTTCACAACCTGGAGTCTTTCACGCTTCTGAGCTACCTTCTTAACTCATGAT 960  
Db 901 GGTTCACAACCTGGAGTCTTTCACGCTTCTGAGCTACCTTCTTAACTCATGAT 960  
QY 961 CTACTGAACTCCAGAGCGCACCCGCTCGGCTGGATGGGCTCGAGAGCGAGCGCG 1020  
Db 961 CTACTGAACTCCAGAGCGCACCCGCTCGGCTGGATGGGCTCGAGAGCGAGCGCG 1020  
QY 1021 CCCCAGGCGCCCTCCGAGGCGCCAGCTCTCACACCCCGGCTGCTGGGCTG 1080  
Db 1021 CCCCAGGCGCCCTCCGAGGCGCCAGCTCTCACACCCCGGCTGCTGGGCTG 1080  
QY 1081 CTGGCAGAAAGGGGCAACCGGAGGCGCATCGCTGCAAGGTATGGGCTGGGTGAGCGCG 1140  
Db 1081 CTGGCAGAAAGGGGCAACCGGAGGCGCATCGCTGCAAGGTATGGGCTGGGTGAGCGCG 1140  
QY 1141 GGTAGCGCTGAGCGCGGAGGCGACCTCGGGGTGGCGTGGGCGGCGCTCGTGGC 1200  
Db 1141 GGTAGCGCTGAGCGCGGAGGCGACCTCGGGGTGGCGTGGGCGGCGCTCGTGGC 1200  
QY 1201 TTTACCCACCTCCAGCTCCGCGCAGCTCTCGAGGCGGCACTGAGAGCGCGCTCACTCAA 1260  
Db 1201 TTTACCCACCTCCAGCTCCGCGCAGCTCTCGAGGCGGCACTGAGAGCGCGCTCACTCAA 1260  
QY 1261 GAGGGCTCCAAGCGCTCGGCTCTCGGCTCTGCTGGAGAGCGCATGAAGTGTGTC 1320  
Db 1261 GAGGGCTCCAAGCGCTCGGCTCTCGGCTCTGCTGGAGAGCGCATGAAGTGTGTC 1320  
QY 1321 CCAGAGCTTCAACCGCGCTTTCGGCTCTCTCGGAGAGGAGTGGCCAGTCCGTGGC 1380  
Db 1321 CCAGAGCTTCAACCGCGCTTTCGGCTCTCTCGGAGAGGAGTGGCCAGTCCGTGGC 1380  
QY 1381 CGTCACTGTGAGCATCTTTTGGCTCTGCTGGGCGCCATACAGCTGTGATGATCATCG 1440  
Db 1381 CGTCACTGTGAGCATCTTTTGGCTCTGCTGGGCGCCATACAGCTGTGATGATCATCG 1440  
QY 1441 GCGCGCTGCCATGCGCACTGCGTCCCTGACTGTGTGTAAGAACTCTTCTGTGCTCT 1500  
Db 1441 GCGCGCTGCCATGCGCACTGCGTCCCTGACTGTGTGTAAGAACTCTTCTGTGCTCT 1500  
QY 1501 GTGGGCGAACTCGGCTGTCAACCTCTCTTACCTCTGTGCGACCAAGCTTCGCGCG 1560  
Db 1501 GTGGGCGAACTCGGCTGTCAACCTCTCTTACCTCTGTGCGACCAAGCTTCGCGCG 1560



QY 1561 GGCCTTCCAGAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGAGCTCCCTGGA 1620  
DB 1561 GGCCTTCCAGAGCTGCTCTGCCCCCAGAGCTCAAAATCCAGCCCCCAGAGCTCCCTGGA 1620  
QY 1621 GCAGTGTGGAGAGTGAAGTGGCCACACAGAGCTCCCTCAGCCACGCTCTCTCAGCCCCAG 1680  
DB 1621 GCAGTGTGGAGAGTGAAGTGGCCACACAGAGCTCCCTCAGCCACGCTCTCTCAGCCCCAG 1680  
QY 1681 GTCTCTGGGCAATCTGGGCTGCTGCTGCCCCCTACCGGCTCGTTCGCCAGGGGTGAGCCC 1740  
DB 1681 GTCTCTGGGCAATCTGGGCTGCTGCTGCCCCCTACCGGCTCGTTCGCCAGGGGTGAGCCC 1740  
QY 1741 GCGCTGTCTGGGCTGCTCTTAATGCCAGGAGCCACCTGCGCATGGAGGCGCTTC 1800  
DB 1741 GCGCTGTCTGGGCTGCTCTTAATGCCAGGAGCCACCTGCGCATGGAGGCGCTTC 1800  
QY 1801 CTGGGTGGCCAGAGGGCCCTCACTGGCTGAGCTGGAGGTGGTGGCGGCCCTGGCC 1860  
DB 1801 CTGGGTGGCCAGAGGGCCCTCACTGGCTGAGCTGGAGGTGGTGGCGGCCCTGGCC 1860  
QY 1861 CCCAATTCTGCTCCACGGGGAGGACAGTCTGGAGTCCACAGCATGTGCCACCC 1920  
DB 1861 CCCAATTCTGCTCCACGGGGAGGACAGTCTGGAGTCCACAGCATGTGCCACCC 1920  
QY 1921 CCGTGTGGTCCACCGCTTCGAGTTACTGGTTGGTGTCTTCCAAAGCAGCACTGG 1980  
DB 1921 CCGTGTGGTCCACCGCTTCGAGTTACTGGTTGGTGTCTTCCAAAGCAGCACTGG 1980  
QY 1981 GTGTGCTCCAGGCTTCTGCCCCCTAGCAGTTTGCCTCTGCAGTGCACACCTGCACACC 2040  
DB 1981 GTGTGCTCCAGGCTTCTGCCCCCTAGCAGTTTGCCTCTGCAGTGCACACCTGCACACC 2040  
QY 2041 CTTGCACACACTGTCACACCGTCTCTCTCCCGGCAAGCCACAGACACTGCTTTGCTG 2100  
DB 2041 CTTGCACACACTGTCACACCGTCTCTCTCCCGGCAAGCCACAGACACTGCTTTGCTG 2100  
QY 2101 CTTTGTCTCTGATAGCTCAGGCTGAGGCTGAGGCTTTCACCCCTTTCACCACTCT 2160  
DB 2101 CTTTGTCTCTGATAGCTCAGGCTGAGGCTGAGGCTTTCACCCCTTTCACCACTCT 2160  
QY 2161 CTCTGCCCCAAAGTGTCAAGGGCCCTTAGGAACTCGAAGCTGTCTCTGCTTTTCA 2220  
DB 2161 CTCTGCCCCAAAGTGTCAAGGGCCCTTAGGAACTCGAAGCTGTCTCTGCTTTTCA 2220  
QY 2221 TTCTGGGTGTTTTCAGAAAGATGAAGAAACATGTCTGAACTTGAATGTCGTGG 2280  
DB 2221 TTCTGGGTGTTTTCAGAAAGATGAAGAAACATGTCTGAACTTGAATGTCGTGG 2280  
QY 2281 ATGTTTAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGTGGATTGGGAGGTGGG 2340  
DB 2281 ATGTTTAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGTGGATTGGGAGGTGGG 2340  
QY 2341 CTCCACAGCCCTCTCCCTCCGCTAAGGCTCCGCTGAGCTGCGAGCTGCTTTCTGCC 2400  
DB 2341 CTCCACAGCCCTCTCCCTCCGCTAAGGCTCCGCTGAGCTGCGAGCTGCTTTCTGCC 2400  
QY 2401 CACCCCGCTCTGGGCTCAACACAGCCCTGGTGGCCAAAGCCTGCCCGGCACTCTGTTT 2460  
DB 2401 CACCCCGCTCTGGGCTCAACACAGCCCTGGTGGCCAAAGCCTGCCCGGCACTCTGTTT 2460  
QY 2461 GCTCACCAGGACCTCTGGGGTGTGGAGAGAGGGGCGGCTGGGCGGAGGGTCC 2520  
DB 2461 GCTCACCAGGACCTCTGGGGTGTGGAGAGAGGGGCGGCTGGGCGGAGGGTCC 2520  
QY 2521 CAAGCGTGCAGGGCGGTTCAGAGAGAGTGGTCCCGGAGAGGGCGCTTCGCAATGTCT 2580  
DB 2521 CAAGCGTGCAGGGCGGTTCAGAGAGAGTGGTCCCGGAGAGGGCGCTTCGCAATGTCT 2580  
QY 2581 GTGCAACCGGTGCCACGCGCTCTGCAATGCTCTCTGCTGTGCCCCGCTGCGCTTGCAT 2640  
DB 2581 GTGCAACCGGTGCCACGCGCTCTGCAATGCTCTCTGCTGTGCCCCGCTGCGCTTGCAT 2640

QY 2641 AACCGTAGGTGCACAAATAAGTGATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA 2699  
DB 2641 AACCGTAGGTGCACAAATAAGTGATTTTTTAAAAAAAAAAAAAAAAAAAAAAAAA 2699  
RESULT 3  
US-09-642-514-5  
; Sequence 5, Application US/09642514  
; Patent No. 6437100  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: ORT1290  
; CURRENT APPLICATION NUMBER: US/09/642,514  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: US 09/167,354  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 2699  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: CDNA  
US-09-642-514-5

Query Match 100.0%; Score 2699; DB 3; Length 2699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCACGCGTCCGCGGCTGCACGCTCGACCGGCGGCTCAGGCTCCGGGTCTCTCTCC 60  
DB 1 CCACGCGTCCGCGGCTGCACGCTCGACCGGCGGCTCAGGCTCCGGGTCTCTCTCC 60  
QY 61 GCTGAGCAGCGGCTGCGGCGGCTCCGCGGCTCGATCCGCGGCGGCGGCGGCGGCA 120  
DB 61 GCTGAGCAGCGGCTGCGGCGGCTCCGCGGCTCGATCCGCGGCGGCGGCGGCGGCA 120  
QY 121 CGCGTGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 180  
DB 121 CGCGTGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCA 180  
QY 181 ACCGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
DB 181 ACCGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
QY 241 CCCAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
DB 241 CCCAGCTCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
QY 301 GGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
DB 301 GGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
QY 361 GGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
DB 361 GGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
QY 421 GGCGCTGTCTATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
DB 421 GGCGCTGTCTATCTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480  
QY 481 CGACTCGAGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
DB 481 CGACTCGAGCTCCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
QY 541 CCTCGTGGCGGCTCTCTGCTATGTATGTATGTATGTATGTATGTATGTATGTATGTAT 600

Db 541 CCTCGTCGGGCTTCTGTCATCCCACTGATGTATGTAACCTACGTGCTGACAGGCGGCTGGAC 600  
Qy 601 CTTTGGCCGGGCTCTGCAAGCTGTGGCTGTGGTGTGAGTACCTGCTGTGACCTCTCTC 660  
Db 601 CTTTGGCCGGGCTCTGCAAGCTGTGGCTGTGGTGTGAGTACCTGCTGTGACCTCTCTC 660  
Qy 661 TGGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCTGGTCAACCGAGCGGTCTC 720  
Db 661 TGGCTTCAACATCGTGTCTCATCAGTACGACCGCTTCTGTGCTGGTCAACCGAGCGGTCTC 720  
Qy 721 ATACCGGGCCAGCAGGCTGTACACCGCGGCGGACGTGCGGAAGATGCTGCTGTGGGT 780  
Db 721 ATACCGGGCCAGCAGGCTGTACACCGCGGCGGACGTGCGGAAGATGCTGCTGTGGGT 780  
Qy 781 GCTGCGCTTCTGCTGTATCGGACCAACCTATCTGAGCTGGGATACCTGTCCGGGGCAG 840  
Db 781 GCTGCGCTTCTGCTGTATCGGACCAACCTATCTGAGCTGGGATACCTGTCCGGGGCAG 840  
Qy 841 CTCATCCCGAGGGCTATGCTATGCGAGTCTTCTTACAACTGGTACTTCTCATCAC 900  
Db 841 CTCATCCCGAGGGCTATGCTATGCGAGTCTTCTTACAACTGGTACTTCTCATCAC 900  
Qy 901 GGCCTTCCACCTGGAGTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAGCAT 960  
Db 901 GGCCTTCCACCTGGAGTCTTTACGCGCTTCTCAGCGTCACTTCTTTAACTCAGCAT 960  
Qy 961 CTACCTGAATCCAGAGCGCACCGCTCCGCGTGTGATGCGGCTCGAGAGCAGCGG 1020  
Db 961 CTACCTGAATCCAGAGCGCACCGCTCCGCGTGTGATGCGGCTCGAGAGCAGCGG 1020  
Qy 1021 CCCGAGCGCTCCCGAGGCTCAGCTCTACACCGCTGCTGCTGGCTGTGGGTG 1080  
Db 1021 CCCGAGCGCTCCCGAGGCTCAGCTCTACACCGCTGCTGCTGGCTGTGGGTG 1080  
Qy 1081 CTGGCAGAGGGCAGCGGAGGCTATGCGCTGACAGGATGCGGTGGGTGAGCGCG 1140  
Db 1081 CTGGCAGAGGGCAGCGGAGGCTATGCGCTGACAGGATGCGGTGGGTGAGCGCG 1140  
Qy 1141 CTTAGCGCTGAGGCGGAGGCGACCTCCGCGGCTGCGGTGGGCGGCTCCGCTGCG 1200  
Db 1141 CTTAGCGCTGAGGCGGAGGCGACCTCCGCGGCTGCGGTGGGCGGCTCCGCTGCG 1200  
Qy 1201 TTTACCCACCTCCAGCTCCGAGCTCTCTCGAGGGCTATGAGAGCGCGCTCACTCAA 1260  
Db 1201 TTTACCCACCTCCAGCTCCGAGCTCTCTCGAGGGCTATGAGAGCGCGCTCACTCAA 1260  
Qy 1261 GAGGGCTTCAAGCGCTGGGCTCTCTCGGCTGCTGAGAGCGCATGAGATGGTGC 1320  
Db 1261 GAGGGCTTCAAGCGCTGGGCTCTCTCGGCTGCTGAGAGCGCATGAGATGGTGC 1320  
Qy 1321 CCAGAGCTTCAACAGCGCTTTGCGCTGTCTCGGACAGGAAGTGGCCAGTCTGCGC 1380  
Db 1321 CCAGAGCTTCAACAGCGCTTTGCGCTGTCTCGGACAGGAAGTGGCCAGTCTGCGC 1380  
Qy 1381 CGTCATCGTGAACATCTTTGGGCTCTGCTGGGCGGCTATACAGCTGTGATCATCCG 1440  
Db 1381 CGTCATCGTGAACATCTTTGGGCTCTGCTGGGCGGCTATACAGCTGTGATCATCCG 1440  
Qy 1441 GCGCGCTTCCATGCGCATGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Db 1441 GCGCGCTTCCATGCGCATGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500  
Qy 1501 GTGGGCCAACTCGGCTGTCAACCGCTGTCTTACCTCTGTGCGCACACAGCTTCCGCG 1560  
Db 1501 GTGGGCCAACTCGGCTGTCAACCGCTGTCTTACCTCTGTGCGCACACAGCTTCCGCG 1560  
Qy 1561 GGCCTTCAACAGCTGTCTGCGCGGCTGAGAGCTCAAAATCCAGCGGCTCAGCTCCGTA 1620  
Db 1561 GGCCTTCAACAGCTGTCTGCGCGGCTGAGAGCTCAAAATCCAGCGGCTCAGCTCCGTA 1620  
Qy 1621 GCATGCTGGAAGTGAAGTGGGCTCCACAGAGCTTCCCTCAGCGCACGCTCTCTCAGCC 1680  
Db 1621 GCATGCTGGAAGTGAAGTGGGCTCCACAGAGCTTCCCTCAGCGCACGCTCTCTCAGCC 1680

RESULT 4

US-08-985-090-1

; Sequence 1, Application US/08985090.

Qy 1681 GTCTCTGGGCATCTGGCCCTCTGCCCCCTACCCGGCTGTTTCCCCCAGAGGTTGAGCCC 1740  
Db 1681 GTCTCTGGGCATCTGGCCCTCTGCCCCCTACCCGGCTGTTTCCCCCAGAGGTTGAGCCC 1740  
Qy 1741 GCGCGTGTCTGTGGGCTCTCTTAATGCGACGGGAGCCACCTGCGCATGGAGGCGGCTTC 1800  
Db 1741 GCGCGTGTCTGTGGGCTCTCTTAATGCGACGGGAGCCACCTGCGCATGGAGGCGGCTTC 1800  
Qy 1801 CTGGGTTGGCAGAGGGCCCTCTACCTGCTGACCTGGAGGCTGGGTGGGCGGCTTGGCC 1860  
Db 1801 CTGGGTTGGCAGAGGGCCCTCTACCTGCTGACCTGGAGGCTGGGTGGGCGGCTTGGCC 1860  
Qy 1861 CCCACATTTCTGGCTCCACCGGGAGGAGCTCTGGAGGTTCCAGACATGCTGCCACCC 1920  
Db 1861 CCCACATTTCTGGCTCCACCGGGAGGAGCTCTGGAGGTTCCAGACATGCTGCCACCC 1920  
Qy 1921 CTTGCTGTGGCCACCTTCCGAGTACTTGGTGTGCTTCTCCAAAGCAAGCACTGG 1980  
Db 1921 CTTGCTGTGGCCACCTTCCGAGTACTTGGTGTGCTTCTCCAAAGCAAGCACTGG 1980  
Qy 1981 GTGCTCTCAGGCTTCTGCGCTAGCAGTTTGGCTCTGCAGCTGCACCTGCACACCTGCACAC 2040  
Db 1981 GTGCTCTCAGGCTTCTGCGCTAGCAGTTTGGCTCTGCAGCTGCACACCTGCACAC 2040  
Qy 2041 CTTGACACACCTGACACCGCTCTCTCCCGGCAAGCCAGGACACTGCTTTGCTG 2100  
Db 2041 CTTGACACACCTGACACCGCTCTCTCTCCCGGCAAGCCAGGACACTGCTTTGCTG 2100  
Qy 2101 CTTGCTGTCTTGTGATGAGCTCAGGCTGGCCCTTTCACCCCTCTTCCCAACCACTCT 2160  
Db 2101 CTTGCTGTCTTGTGATGAGCTCAGGCTGGCCCTTTCACCCCTCTTCCCAACCACTCT 2160  
Qy 2161 CTCTGCCCCAAAAGTGTCAAGGGCCCTAGGAACTCTGAACTGTTCTCTCTTTTCCA 2220  
Db 2161 CTCTGCCCCAAAAGTGTCAAGGGCCCTAGGAACTCTGAACTGTTCTCTCTTTTCCA 2220  
Qy 2221 TTTCTGGGTGTTTTTCAGAAAGATGAGAAAGAAACAATGTCTGTGAATTTGATGTT 2280  
Db 2221 TTTCTGGGTGTTTTTCAGAAAGATGAGAAAGAAACAATGTCTGTGAATTTGATGTT 2280  
Qy 2281 ATGTTTAAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGCTGATTTGGCAGGTGGG 2340  
Db 2281 ATGTTTAAATCAAGAGAGACAAATTTGCTGAGAGCTCAGGGCTGATTTGGCAGGTGGG 2340  
Qy 2341 CTCCACGCGCTCTCTCCCTCCGCTAAAGCTTCCGCTGAGCTGTGCCAGCTCTTCTGCC 2400  
Db 2341 CTCCACGCGCTCTCTCCCTCCGCTAAAGCTTCCGCTGAGCTGTGCCAGCTCTTCTGCC 2400  
Qy 2401 CACCCGCGCTCTGGGCTCACACCGCTGTGGGCAAGCCCTGCCCCCGGCCACTCTGTTT 2460  
Db 2401 CACCCGCGCTCTGGGCTCACACCGCTGTGGGCAAGCCCTGCCCCCGGCCACTCTGTTT 2460  
Qy 2461 GCTCAACCGAGCTCTGGGGTTGTTGGAGGAGGGGCGCGGCTGGGCGCGAGGGTCC 2520  
Db 2461 GCTCAACCGAGCTCTGGGGTTGTTGGAGGAGGGGCGCGGCTGGGCGCGAGGGTCC 2520  
Qy 2521 CAAGGCTGAGGGGCGGTCCAGAGGAGGTGCGGGGAGGGGCGGCTTCCGCAATGTGCT 2580  
Db 2521 CAAGGCTGAGGGGCGGTCCAGAGGAGGTGCGGGGAGGGGCGGCTTCCGCAATGTGCT 2580  
Qy 2581 GTGCACCGCTGCCAGCGCTCTGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 2640  
Db 2581 GTGCACCGCTGCCAGCGCTCTGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 2640  
Qy 2641 AACCGTGAAGTCAATAAAGTGTATTTTTTAAAAAATAAAAAAATAAAAAAATAAAAA 2699  
Db 2641 AACCGTGAAGTCAATAAAGTGTATTTTTTAAAAAATAAAAAAATAAAAAAATAAAAA 2699

Patent No. 5885893  
GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl  
TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
NUMBER OF SEQUENCES: 28  
CORRESPONDENCE ADDRESS:  
ADDRESSES: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,090  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jean M. Silveri  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2689 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 291..1625  
US-08-985-090-1

Query Match 97.6%; Score 2635.2; DB 2; Length 2689;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
QY 25 CGCACCGGCGGCTCAGGCTCCGGCTCCTCTCCGGCTGCAGACGCGCGCTGCCGGCC 84  
DB 18 CGCACCGGCGGCTCAGGCTCCGGCTCCTCTCCGGCTGCAGACGCGCGCTGCCGGCC 77  
QY 85 CCACCTGGGCTCGGATCCGGCCCGCGCCCTCTCCGGCACCGCTGCTCTGGCCCGCGCCG 144  
DB 78 CCACCTGGGCTCGGATCCGGCCCGCGCCCTCTCCGGCACCGCTGCTCTGGCCCGCGCCG 137  
QY 145 GCCCGCGGACCATCGCTGGCGGCGCCCGCGAGGGAAACCGACCGCGCGCGCGCCGCA 204  
DB 138 GCCCGCGGACCATCGCTGGCGGCGCCCGCGAGGGG-AAACCGACCGCGCGCGCGCGCA 196  
QY 205 AAGACGAGGCTCCCGGGCGCGGCGCCCTCTCCGGCGCGCGCGCTCTCGGCGCGCGCTGC 264  
DB 197 AAGACGAGGCTCCCGGGCGCGGCGCCCTCTCCGGCGCGCGCGCTCTCGGCGCGCGCTGC 256  
QY 265 CCGCGTCCCGAGCGCGCTGAGCTGCGGGGCGCATGAGACGCGCGCGCGCGCGCGCGCGCC 324  
DB 257 CCGCGTCCCGAGCGCGCTGAGCTGCGGGGCGCATGAGACGCGCGCGCGCGCGCGCGCG 316  
QY 325 GCTGAACGCTTCGGGGCGCTCGCGGGGAGATCGCGGCGGCGCGGCGCGCGCGCGGCTT 384  
DB 317 GCTGAACGCTTCGGGGCGCTCGCGGGGAGAGCGCGCGCGCGCGCGCGCGCGCGGCTT 376  
QY 385 CTCGCGAGCTGGACCGGGGCTGCTGGCGCGCTCATGGCGCTGCTCATGCTGGCGCACGCT 444  
DB 377 CTCGCGAGCTGGACCGGGGCTGCTGGCGCGCTCATGGCGCTGCTCATGCTGGCGCACGCT 436

QY 445 GCTGGGCAACGGCGTGGTCTATGCTCGCTTCTGTCGCCGACTCGAGCCTCCGACCCAGAA 504  
DB 437 GCTGGGCAACGGCGTGGTCTATGCTCGCTTCTGTCGCCGACTCGAGCCTCCGACCCAGAA 496  
QY 505 CAACCTTCTTCTGCTCAACCTCGGCATCTCGCATCTCTGTCGGCGGCTTCTGTCATCC 564  
DB 497 CAACCTTCTTCTGCTCAACCTCGGCATCTCGCATCTCTGTCGGCGGCTTCTGTCATCC 556  
QY 565 ACTGTATGTACCTACCTGCTGACAGGCGCTGGAACCTTCGGCCGGGCGCTTCTGCAAGCT 624  
DB 557 ACTGTATGTACCTACCTGCTGACAGGCGCTTGGACCTTCGGCCGGGCGCTTCTGCAAGCT 616  
QY 625 GTGGCTGTAGTGAAGTACCTGCTGTGCAACCTCTCTGCTTCAACATCTGCTCATCAG 684  
DB 617 GTGGCTGTAGTGAAGTACCTGCTGTGCAACCTCTCTGCTTCAACATCTGCTCATCAG 676  
QY 685 CTACGACCGCTTCTGTCGGTCAACCGAGCGCTCTATACCGGGCCAGAGGGGTGACAC 744  
DB 677 CTACGACCGCTTCTGTCGGTCAACCGAGCGCTCTATACCGGGCCAGAGGGGTGACAC 736  
QY 745 GCGCGGCGAGTGGGGAAGATGCTGCTGTGTGGGTGCTGCGCTTCTGCTGTACGGACC 804  
DB 737 GCGCGGCGAGTGGGGAAGATGCTGCTGTGTGGGTGCTGCGCTTCTGCTGTACGGACC 796  
QY 805 AGCCATCTGAGTGGGAGTACCTGCTCGGGGGAGCTTCCATCCCGAGGGGCACTGCTA 864  
DB 797 AGCCATCTGAGTGGGAGTACCTGCTCGGGGGAGCTTCCATCCCGAGGGGCACTGCTA 856  
QY 865 TGCCGAGTCTTCTACAACTGCTTCTCTCATACGGCTTCCACCTTGGAGTCTTTTAC 924  
DB 857 TGCCGAGTCTTCTACAACTGCTTCTCTCATACGGCTTCCACCTTGGAGTCTTTTAC 916  
QY 925 GCCCTTCTCAGCGTCACTTCTTTAACTCAGCATCTACCTGAACATCTCAGAGCGCAC 984  
DB 917 GCCCTTCTCAGCGTCACTTCTTTAACTCAGCATCTACCTGAACATCTCAGAGCGCAC 976  
QY 985 CCGCTCCGGCTGAGTGGGGCTCGAGAGCGAGCGCGCGCGCGCGCGCGCTCCCGAGGCCA 1044  
DB 977 CCGCTCCGGCTGAGTGGGGCTCGAGAGCGAGCGCGCGCGCGCGCGCGCTCCCGAGGCCA 1036  
QY 1045 GCCCTCACACCCCGCGCTGCTGGGTGCTGGGAGAGAGGGGCGACCGGGAGGC 1104  
DB 1037 GCCCTCACACCCCGCGCTGCTGGGTGCTGGGAGAGAGGGGCGACCGGGAGGC 1096  
QY 1105 CATGCGCTGCACAGGTATGGGTGGGTGAGCGCGCTAGCGCTGAGCGCGGGAGGC 1164  
DB 1097 CATGCGCTGCACAGGTATGGGTGGGTGAGCGCGCTAGCGCTGAGCGCGGGAGGC 1156  
QY 1165 GACCTCGGGGTGGCGTGGGGGGCGCTCGTGGCTTCAACCTCAGCTCCGGCAG 1224  
DB 1157 GACCTCGGGGTGGCGTGGGGGGCGCTCGTGGCTTCAACCTCAGCTCCGGCAG 1216  
QY 1295 CTCTCGAGGGGCACTGAGAGCGCGCTCACTAAGAGGGGCTCCAGACCGCTCGCGCTC 1284  
DB 1217 CTCTCGAGGGGCACTGAGAGCGCGCTCACTAAGAGGGGCTCCAGACCGCTCGCGCTC 1276  
QY 1285 CTGCGCTCGTGGAGAGCGCATGAAGATGCTGTCAGAGCTTCAACCGAGCTTTG 1344  
DB 1277 CTGCGCTCACTGGAGAGCGCATGAAGATGCTGTCAGAGCTTCAACCGAGCTTTG 1336  
QY 1345 GCTGTCTGGGACAGGAAGTGGCCAGTCTGCTGGCGCTCATCTGAGCATCTTTGGCT 1404  
DB 1337 GCTGTCTGGGACAGGAAGTGGCCAGTCTGCTGGCGCTCATCTGAGCATCTTTGGCT 1396  
QY 1405 CTGCTGGGCGCCATACACGCTGCTGATCATCTCGGGCGCGCTGCCATGGCCACTGGT 1464  
DB 1397 CTGCTGGGCGCCATACACGCTGCTGATGATCATCTCGGGCGCGCTGCCATGGCCACTGGT 1456  
QY 1465 CCCTGACTACTGGTACGAAACCTCTTCTGCTCTGCTGGGCGCAACTCGGCTGTCAACCC 1524  
DB 1457 CCCTGACTACTGGTACGAAACCTCTTCTGCTCTGCTGGGCGCAACTCGGCTGTCAACCC 1516

1525 TGCTCTACCTCTGTGTCACACAGCTTCGCGCGGGCTTCACCAAGCTGCTCTGCCC 1584  
Db  
1517 TGCTCTACCTCTGTGTCACACAGCTTCGCGCGGGCTTCACCAAGCTGCTCTGCCC 1576  
Qy  
1585 CCAGAAAGCTCAAAATCCAGCCCCACAGCTCCCTGTGAGCACTGCTGGAAGTGAAGTGCCCA 1644  
Db  
1577 CCAGAAAGCTCAAAATCCAGCCCCACAGCTCCCTGTGAGCACTGCTGGAAGTGAAGTGCCCA 1636  
Qy  
1645 CCAGAGCTCTCTAGCCACAGCTCTCTCAGCCCCAGGTTCTCTGGGCATCTGGCCCTGCT 1704  
Db  
1637 CCAGAGCTCTCTAGCCACAGCTCTCTCAGCCCCAGGTTCTCTGGGCATCTGGCCCTGCT 1696  
Qy  
1705 GCCCTCTACCGGCTGCTTCCCGCAGGGGTGAGCCCCCGCGTGTCTGTGGCCCTCTCTTA 1764  
Db  
1697 GCCCTCTACCGGCTGCTTCCCGCAGGGGTGAGCCCCCGCGTGTCTGTGGCCCTCTCTTA 1756  
Qy  
1765 ATGCCAGGACCCACCTGCTGATGAGGCGCTTCTGGGTTGGCAGAGGGCCCTCA 1824  
Db  
1757 ATGCCAGGACCCACCTGCTGATGAGGCGCTTCTGGGTTGGCAGAGGGCCCTCA 1816  
Qy  
1825 CTGGCTGGAATGGAGGCTGGGTGGCGGCCCTTGCCCCCACAATCTTGGCTCCACCGGGA 1884  
Db  
1817 CTGGCTGGAATGGAGGCTGGGTGGCGGCCCTTGCCCCCACAATCTTGGCTCCACCGGGA 1875  
Qy  
1885 GGGACAGCTGAGGTCAGACATGCTGCCACCCCTGCTGTGGTGGCCACCTTCGCGAG 1944  
Db  
1876 GGGACAGCTGAGGTCAGACATGCTGCCACCCCTGCTGTGGTGGCCACCTTCGCGAG 1935  
Qy  
1945 TTACTGTTGGTGTCTTCCCAAGCAAGCACTGGGTGTGCTCCAGGCTTCTGCCCTA 2004  
Db  
1936 TTACTGTTGGTGTCTTCCCAAGCAAGCACTGGGTGTGCTCCAGGCTTCTGCCCTA 1995  
Qy  
2005 GCAGTTTGGCTCTGCAAGCTGCAACCTTGCAACCCCTTGCAACCTTGCAACCCCTGCA 2064  
Db  
1996 GCAGTTTGGCTCTGCAAGCTGCAACCTTGCAACCCCTTGCAACCTTGCAACCCCTGCA 2055  
Qy  
2065 CTCTCCCGGCAAGCCAGCACTGCTGCTTGGTGTGCTTGTCTTGTGCAATAGCTTC 2124  
Db  
2056 CTCTCCCGGCAAGCCAGCACTGCTGCTTGGTGTGCTTGTCTTGTGCAATAGCTTC 2115  
Qy  
2125 AGGCTGCGCTTTCACCCCTCTCCCAAGCACTGCTGCTGCGCCCAAGGTCAAGG 2184  
Db  
2116 AGGCTGCGCTTTCACCCCTCTCCCAAGCACTGCTGCTGCGCCCAAGGTCAAGG 2175  
Qy  
2185 GGCCTAGGAACCTGCAAGCTGTTCTCTGCTTTCATCTGGGTGTTTCAAGAAAGTGA 2244  
Db  
2176 GGCCTAGGAACCTGCAAGCTGTTCTCTGCTTTCATCTGGGTGTTTCAAGAAAGTGA 2235  
Qy  
2245 AGAAGAAACATGTCTGTGAATTTGATGTTCTGGGATGTTTAAATCAAGAGAGACAAAT 2304  
Db  
2236 AGAAGAAACATGTCTGTGAATTTGATGTTCTGGGATGTTTAAATCAAGAGAGACAAAT 2295  
Qy  
2305 TGCTAGGAGCTCAGGCTGGATGGCAGGTGGGCTCCACGCGCTCTCTCCCTCGCT 2364  
Db  
2296 TGCTAGGAGCTCAGGCTGGATGGCAGGTGGGCTCCACGCGCTCTCTCCCTCGCT 2355  
Qy  
2365 AAGGCTTCGGGTGAGCTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2424  
Db  
2356 AAGGCTTCGGGTGAGCTGTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2415  
Qy  
2425 GCCCTGGTGGCAAGCTGCCCCCGGCACTGTTTGTGCTCACCCAGGACCTCTGGGGGTT 2484  
Db  
2416 GCCCTGGTGGCAAGCTGCCCCCGGCACTGTTTGTGCTCACCCAGGACCTCTGGGGGTT 2475  
Qy  
2485 GTTGGGAGAGGGGGCCCGGCTGGGCGCAGAGGTTCAGAGGTGGGCGGTTCAGAG 2544  
Db  
2476 GTTGGGAGAGGGGGCCCGGCTGGGCGCAGAGGTTCAGAGGTGGGCGGTTCAGAG 2535  
Qy  
2545 GGAGTGGCCGGGAGGGGGCCGCTTGGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2604  
Db  
2536 GGAGTGGCCGGGAGGGGGCCGCTTGGCCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 2595  
Qy  
2605 ATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2664

## RESULT 5

US-09-165-543-1

; Sequence 1, Application US/09165543

; Patent No. 6093545

; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman

; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor

; NUMBER OF SEQUENCES: 39

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE &amp; COCKFIELD, LLP

; STREET: 28 State Street

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09165,543

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/042,780

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Elizabeth A. Hanley

; REGISTRATION NUMBER: 33,505

; REFERENCE/DOCKET NUMBER: MMI-032CP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617)227-7400

; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 2689 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 291..1625

US-09-165-543-1

Query Match 97.6%; Score 2635.2; DB 3; Length 2689;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2659; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 25 GCACCGGAGCGGCTCAGGCTCCGGCTCTCTCCGCTGACGAGCGCGGCTGCGGCC 84

Db 18 GCACCGGAGCGGCTCAGGCTCCGGCTCTCTCCGCTGACGAGCGCGGCTGCGGCC 77

Qy 85 CCACCTGGGCTCGGATCCCGGCCCCCGGCCCCCTCGGCAACGCTGCTCTGGCCCCGGCCG 144

Db 78 CCACCTGGGCTCGGATCCCGGCCCCCGGCCCCCTCGGCAACGCTGCTCTGGCCCCGGCCG 137

Qy 145 GCCCGCGGACCATCGCTGGGCGCCCCCGGAGGGGAAACCCGACCCGGCCCAAGGGCCCGCA 204

Db 138 GCCCGCGGACCATCGCTGGGCGCCCCCGGAGGGG-AAACCCGACCCGGCCCAAGGGCCCGCA 196

Qy 205 AAGACGAGGCTCCCGGG 264

Db 197 AAGACGAGGCTCCCGGG 256

QY 265 CCGCGTCCCGAGCCGCTGAGCCTTGGGGCCCATGGAGCGCGCGCCGCGAGCGGCG 324  
Db 257 CCGCGTCCCGAGCCGCTGAGCCTTGGGGCCCATGGAGCGCGCGCCGCGAGCGGCG 316  
QY 325 GCTGAACGCTTCGGGGCGCTGGCGGGGATATCGCGCGCGGGCGGGCGCGCGGCTT 384  
Db 317 GCTGAACGCTTCGGGGCGCTGGCGGGGAGCGGGCGGGCGGGCGGGCGGCTT 376  
QY 385 CTCGGAGCCTGGACCGCGGCTGGCGCGCTCATGGCGCTGCTCATGGTGGCCACGGT 444  
Db 377 CTCGGAGCCTGGACCGCGGCTGGCGCGCTCATGGCGCTGCTCATGGTGGCCACGGT 436  
QY 445 GCTGGGCAACGGCTGCTATGCTCGCCTTCGTGGCCGACTCGAGCCTCGCACCCAGAA 504  
Db 437 GCTGGGCAACGGCTGCTATGCTCGCCTTCGTGGCCGACTCGAGCCTCGCACCCAGAA 496  
QY 505 CAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTGTCGGCGGCTTCGTGATCCC 564  
Db 497 CAACTTCTTCCTGCTCAACCTCGCCATCTCCGACTTCCTGTCGGCGGCTTCGTGATCCC 556  
QY 565 ACTGATGATACCTTACGTGCTGACAGGCGCTGGACCTTCGGCCGGGGCTTCGAAAGCT 624  
Db 557 ACTGATGATACCTTACGTGCTGACAGGCGCTGGACCTTCGGCCGGGGCTTCGAAAGCT 616  
QY 625 GTGGCTGGTGGACTACCTGCTGTGCACCTCTCTGCTTCAACATGCTGCTCATCAG 684  
Db 617 GTGGCTGGTGGACTACCTGCTGTGCACCTCTCTGCTTCAACATGCTGCTCATCAG 676  
QY 685 CTACGACCGCTTCCTGCTCGGTCAACCGAGCGGTCTCATACCGGGCCAGAGGGTGACAC 744  
Db 677 CTACGACCGCTTCCTGCTCGGTCAACCGAGCGGTCTCATACCGGGCCAGAGGGTGACAC 736  
QY 745 GCGCGGGCAGTGGCGGAAGATGCTGCTGTGTGGTGTGCTGCTTCTGCTGTATCGGACC 804  
Db 737 GCGCGGGCAGTGGCGGAAGATGCTGCTGTGTGGTGTGCTGCTTCTGCTGTACGGACC 796  
QY 805 AGCCATCTGAGCTGGGAGTACTCTCGGGGGGAGCTCCATCCCGAGGGCCACTGCTA 864  
Db 797 AGCCATCTGAGCTGGGAGTACTCTCGGGGGGAGCTCCATCCCGAGGGGCACTGCTA 856  
QY 865 TGCCGAGTTCCTTACAACTGTACTTCTCATACAGGCTTCACACCTCGGAGTTCCTTAC 924  
Db 857 TGCCGAGTTCCTTACAACTGTACTTCTCATACAGGCTTCACACCTCGGAGTTCCTTAC 916  
QY 925 GCGCTTCCTCAGGCTCACCTTTAACTCAGATCTACCTGAAATCATCAGAGGGCCAC 984  
Db 917 GCGCTTCCTCAGGCTCACCTTTAACTCAGATCTACCTGAAATCATCAGAGGGCCAC 976  
QY 985 CCGCTTCGGCTGGATGGGCTCGAGGCGAGCGCGCCCGAGCCCTCCCGAGGGCCA 1044  
Db 977 CCGCTTCGGCTGGATGGGCTCGAGAGGAGCGCGCGCCCGAGCCCTCCCGAGGGCCA 1036  
QY 1045 GCGCTCACCAACCCGCTGGCTGCTGGGGCTGCTGGGAGAGGGGCAAGGGAGGCG 1104  
Db 1037 GCGCTCACCAACCCGCTGGCTGCTGGGGCTGCTGGGAGAGGGGCAAGGGAGGCG 1096  
QY 1105 CATGCCGCTGACAGTATGGGGTGGGTGAGCGCGCTGAGCGCTGAGGGCGGGAGGCG 1164  
Db 1097 CATGCCGCTGACAGTATGGGGTGGGTGAGCGCGCTGAGCGCTGAGGGCGGGAGGCG 1156  
QY 1165 GACCTTCGGGGTGGGGTGGGGGGGCTCCGTGGCTTCACCCACTCCAGCTCCGGGAG 1224  
Db 1157 GACCTTCGGGGTGGGGTGGGGGGGCTCCGTGGCTTCACCCACTCCAGCTCCGGGAG 1216  
QY 1225 CTCCTCGAGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTCAAGCGCTCGCGCTC 1284  
Db 1217 CTCCTCGAGGGCACTGAGAGGCGCGCTCACTCAAGAGGGGCTCAAGCGCTCGCGCTC 1276  
QY 1285 CTCGCGCTCGCTGGAGAGCGCATGAAGATGTGTCCAGAGCTTCAACCGGCTTTGG 1344  
Db 1277 CTCGCGCTCACTGGAGAGCGCATGAAGATGTGTCCAGAGCTTCAACCGGCTTTGG 1336

QY 1345 GCTGTCTCGGACGAGAAAGTGGCAAGTCTGCTGGCGCTCATCGTAGCATCTTTGGGCT 1404  
Db 1337 GCTGTCTCGGACGAGAAAGTGGCCAGTCTGCTGGCGCTCATCGTAGCATCTTTGGGCT 1396  
QY 1405 CTGCTGGGCCCCATACACGCTGCTGATGATCATCGGGCGGCTGCGCATGAGCCATGGGT 1464  
Db 1397 CTGCTGGGCCCCATACACGCTGCTGATGATCATCGGGCGGCTGCGCATGAGCCATGGGT 1456  
QY 1465 CCCTGACTACTGCTGATGAAACCTCTCTGCTGCTCTGCTGGGCACTCGGCTGTCAACC 1524  
Db 1457 CCCTGACTACTGCTGATGAAACCTCTCTGCTGCTCTGCTGGGCACTCGGCTGTCAACC 1516  
QY 1525 TGTCTCTTACCTCTGTCGCCACACAGCTTCGCGCGGCTTCAACAAAGCTGCTGCGCC 1584  
Db 1517 TGTCTCTTACCTCTGTCGCCACACAGCTTCGCGCGGCTTCAACAAAGCTGCTGCGCC 1576  
QY 1585 CCAGAAGCTCAAAATCCAGCCCCACAGCTCCCTGAGACACTGCTGGAAGTGAAGTGGCCCA 1644  
Db 1577 CCAGAAGCTCAAAATCCAGCCCCACAGCTCCCTGAGACACTGCTGGAAGTGAAGTGGCCCA 1636  
QY 1645 CCAGAGCTCTCTGAGCCACGCTCTCTCAGCCACAGCTCTCTGAGGCACTGAGGCGCTGCT 1704  
Db 1637 CCAGAGCTCTCTGAGCCACGCTCTCTCAGCCACAGCTCTCTGAGGCACTGAGGCGCTGCT 1696  
QY 1705 GCCCTTACCCTGCTGTTCCCGAGGGGTGAGCCCGCGCTGCTGAGGCGCTCTCTTA 1764  
Db 1697 GCCCTTACCCTGCTGTTCCCGAGGGGTGAGCCCGCGCTGCTGAGGCGCTCTCTTA 1756  
QY 1765 ATGCCACGGCAGCCACCTGCTGAGGCGCTTCTCTGGGTGAGCCAGAGGCGGCTCTCA 1824  
Db 1757 ATGCCACGGCAGCCACCTGCTGAGGCGCTTCTCTGGGTGAGCCAGAGGCGGCTCTCA 1816  
QY 1825 CTGGCTGAGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 1884  
Db 1817 CTGGCTGAGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 1875  
QY 1885 GGGACAGTCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 1944  
Db 1876 GGGACAGTCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 1935  
QY 1945 TTACTGTTGGTGTCTTCCCAAGCAAGCACTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 2004  
Db 1936 TTACTGTTGGTGTCTTCCCAAGCAAGCACTGCTGAGGCTGCTGAGGCTGCTGAGGCTGCT 1995  
QY 2005 GCAGTTGCTCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2064  
Db 1996 GCAGTTGCTCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2055  
QY 2065 CTCTCCCGGCAAGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2124  
Db 2056 CTCTCCCGGCAAGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2115  
QY 2125 AGGCTGCGGCTTTCACCCCTCTTCCCAAGCAAGCACTGCTGAGGCTGCTGAGGCTGCT 2184  
Db 2116 AGGCTGCGGCTTTCACCCCTCTTCCCAAGCAAGCACTGCTGAGGCTGCTGAGGCTGCT 2175  
QY 2185 GCGCTGAGGAACTGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2244  
Db 2176 GCGCTGAGGAACTGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2235  
QY 2245 AGAAGAAACATGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2304  
Db 2236 AGAAGAAACATGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTGAGGCGG 2295  
QY 2305 TGCTGAGGAGCTCAGGCTGAGGCTGAGGCGGCTGAGGCGGCTGAGGCGGCTTCCAGCGGCTTCCCTCCGCT 2364  
Db 2296 TGCTGAGGAGCTCAGGCTGAGGCTGAGGCGGCTGAGGCGGCTTCCAGCGGCTTCCCTCCGCT 2355  
QY 2365 AAGGCTTCGGCTGAGCTGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCCTCCGCT 2424  
Db 2356 AAGGCTTCGGCTGAGCTGAGGCGGCTTCCAGCGGCTTCCAGCGGCTTCCCTCCGCT 2415  
QY 2425 GCGCTGAGGCGCAAGCGCTGCGCGGCGCACTGCTGTTGCTCAGCCAGGAGCTCTGAGGCGGCT 2484

[illegible]

RESULT 6  
US-09-949-016-5059  
; Sequence 5059, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5059  
; LENGTH: 2665  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5059

Query Match	97.6%;	Score 2633.6;	DB 4;	Length 2665;	
Best Local Similarity	99.8%;	Pred. No. 0;			
Matches 2658;	Conservative	0;	Mismatches 4;	Indels 2;	Gaps 2;
QY	10	CGCGCGCTGCACGGTCGACCGGACGCGGCTCAGGCTCCGGCTCCCTCTCCCGCTGCAGCA	69		
Db	4	CTCCGGCTGCACGGTCGACCGGACGCGGCTCAGGCTCCGGCTCCCTCTCCCGCTGCAGCA	63		
QY	70	GCGCGGCTGC CGGCGCCCACTCGGCTCGGATCCGGCCCGCGCCCTCGGACCGCCTGTCT	129		
Db	64	GCGCGGCTGC CGGCGCCCACTGGGCTCGGATCCGGCCCGCGCCCTCGGACCGCCTGTCT	123		
QY	130	CTGGCGCTCGGCGCCCGGCGCCCGGAGACATGCGCTTGGGGCGCCCTCAGGGGAAACCGGACCC	189		
Db	124	CTGGCGCTCGGCGCCCGGCGCCCGGAGACATGCGCTTGGGGCGCCCTCAGGGG-AAACCGGACCC	182		
QY	190	GSCCAAGGCGCCGCAAAACAGAGGCTCCGGGCGGGGCGCCCTCCCGGCGCGCCACGCTCT	249		
Db	183	GSCCAAGGCGCCGCAAAACAGAGGCTCCGGGCGGGGCGCCCTCCCGGCGCGCCACGCTCT	242		
QY	250	CGGCGCGGCGCCTGTGCCCGCGCTCCCGGAGCGCGCTGAGCCTTGGGGGCGCATGGAGGCGCG	309		
Db	243	CGGCGCGGCGCCTGTGCCCGCGCTCCCGGAGCGCGCTGAGCCTTGGGGGCGCATGGAGGCGCG	302		
QY	310	GCGCGCCGACGGGCGCGTGAAACGCTTTCGGGGGCGCTCGCGGGCGATGTCGGCGCGCGCGGG	369		
Db	303	GCGCGCCGACGGGCGCGTGAAACGCTTTCGGGGGCGCTCGCGGGGAGCGCGCGCGCGCGGG	362		

1443 CCATGGCCACTCGTCCCTGACTACTGTGTACGAAACCTCTTCTGGCTCTCTGGTGGCCAA 1502  
1510 CTCGGCTGTCAACCTCTGCTTACCTCTGTGTGACACACAGCTTCGCGCGGCTTTCAC 1569  
1503 CTCGGCTGTCAACCTCTGCTTACCTCTGTGTGACACACAGCTTCGCGCGGCTTTCAC 1562  
1570 CAAGCTGTCTGCCGCCAGAGCTCAAAATCCAGCCCAACAGCTCCCTGGAGCAGCTGTG 1629  
1563 CAAGCTGTCTGCCGCCAGAGCTCAAAATCCAGCCCAACAGCTCCCTGGAGCAGCTGTG 1622  
1630 GAAGTGTGTGCGCCACACAGAGCTCCCTCAGCCACAGCTCTCTCAGCCAGCTCTCTGG 1689  
1623 GAAGTGTGTGCGCCACACAGAGCTCCCTCAGCCACAGCTCTCTCAGCCAGCTCTCTGG 1682  
1690 GCATCTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1749  
1683 GCATCTGCGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1742  
1750 TGTGGCCCTCTCTTAATGCCAGGAGCCACCTGCCATGGAGGCGCTTCTGCTGGTGG 1809  
1743 TGTGGCCCTCTCTTAATGCCAGGAGCCACCTGCCATGGAGGCGCTTCTGCTGGTGG 1802  
1810 CCAGAGGCGCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1869  
1803 CCAGAGGCGCCCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1862  
1870 TGGCTCCACCGGGAGGAGCAGCTGTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAG 1929  
1863 TGGCTCCACC-GGGAGGAGCAGCTGTGAGGTGCTGAGGTGCTGAGGTGCTGAGGTGCTGAG 1921  
1930 GCCACCCCTTCCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1989  
1922 GCCACCCCTTCCAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1981  
1990 AGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2049  
1982 AGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2041  
2050 ACTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2109  
2042 ACTGACACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2101  
2110 TCTTCATAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2169  
2102 TCTTCATAAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2161  
2170 CAAAAGTGTCAAGGGGCTTAGGAACTCTGAAAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTG 2229  
2162 CAAAAGTGTCAAGGGGCTTAGGAACTCTGAAAGCTGTTCTGCTGCTGCTGCTGCTGCTGCTG 2221  
2230 TTTTCAGAAAGATGAAGAAAGAAACATGTCTGTGAATGATGTTGCTGCTGCTGCTGCTGCTG 2289  
2222 TTTTCAGAAAGATGAAGAAAGAAACATGTCTGTGAATGATGTTGCTGCTGCTGCTGCTGCTG 2281  
2290 CAAGAGACAAAATTGCTGAGAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2349  
2282 CAAGAGACAAAATTGCTGAGAGCTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2341  
2350 CTTCTCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2409  
2342 CTTCTCTCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2401  
2410 TCTGGGCTCACAACAGCCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2469  
2402 TCTGGGCTCACAACAGCCCTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2461  
2470 GGACCTCTGGGGGTTGTTGGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2529  
2462 GGACCTCTGGGGGTTGTTGGAGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2521  
2530 CAGGGGCGGTCCAGAGGAGGTGCCCGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2589

2522 CAGGGGCGGTCCAGAGGAGGTGCCCGGGGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 2581  
2590 TGGCAGCGGCTTGCATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2649  
2582 TGGCAGCGGCTTGCATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2641  
2650 GTCACAATAAAAGTGTATTTTTTTA 2673  
2642 GTCACATATAAGTGTATTTTTTTA 2665

RESULT 7  
US-09-949-016-16801  
; Sequence 16801, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE OF INVENTION: 2000-04-14  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16801  
; LENGTH: 9293  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16801

Query Match 72.2%; Score 1947.8; DB 4; Length 9293;  
Best Local Similarity 98.8%; Pred. No. 0;  
Matches 1972; Conservative 0; Mismatches 22; Indels 1; Gaps 1;

QY 679 CATCAGCTACGACCGCTTCTGTCGGTCAACCGAGCGTCTCATACCGGGCCAGCAGGG 738  
DB 5299 CTTCCGCGCGCCCTGACACGCTGCTGTCAGGCTCTCATACCGGGCCAGCAGGG 5358  
QY 739 TGACACGCGGGGCGAGTCCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 798  
DB 5359 TGACACGCGGGGCGAGTCCGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5418  
QY 799 CGGACCGACCTCTGAGCTGGAGTACCTGTCGGGGGCGAGCTCATCCCCGAGGGCCA 858  
DB 5419 CGGACCGACCTCTGAGCTGGAGTACCTGTCGGGGGCGAGCTCATCCCCGAGGGCCA 5478  
QY 859 CTGCTATGCGAGTCTTCTACAACTGCTATCTCTCATACCGCTTCAACCTCGAGTT 918  
DB 5479 CTGCTATGCGAGTCTTCTACAACTGCTATCTCTCATACCGCTTCAACCTCGAGTT 5538  
QY 919 CTTTACGCGCTTCTCAGGCTCACTCTTTTAACTCAGCATCTACCTGACATCCAGAG 978  
DB 5539 CTTTACGCGCTTCTCAGGCTCACTCTTTTAACTCAGCATCTACCTGACATCCAGAG 5598  
QY 979 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCG 1038  
DB 5599 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 5658  
QY 1039 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 1098  
DB 5659 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 5718  
QY 1099 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 1158  
DB 5719 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 5778  
QY 1159 GCGCACCGGCTCCGGCTGGATGGGCTCGAGAGGAGCGCGCGCGCGCGCGCGCGCGCGCG 1218



Db 5779 GGAGGCGACCCCTCGGGGGTGGGGGCGGCTCCGTTGGCTTCAACACCTCCAGCTC 5838  
QY 1219 CGGCACTCTCGAGGGGCACTGAGAGGCGGGCTCACTCAAGAGGGGCTCAAGCCGTC 1278  
Db 5839 CGGCACTCTCGAGGGGCACTGAGAGGCGGGCTCACTCAAGAGGGGCTCAAGCCGTC 5898  
QY 1279 GCGCTCTCGGCTCGCTGAGAGGCGCATGAGATGTTGTCCTCAGAGCTTCAACCCAGCG 1338  
Db 5899 GCGCTCTCGGCTCACTGAGAGGCGCATGAGATGTTGTCCTCAGAGCTTCAACCCAGCG 5958  
QY 1339 CTTTCGGCTGTCTCGGACAGAAAGTGGCCAAAGTGGCTGGCGCTCATCGTAGCATCTT 1398  
Db 5959 CTTTCGGCTGTCTCGGACAGAAAGTGGCCAAAGTGGCTGGCGCTCATCGTAGCATCTT 6018  
QY 1399 TGGGCTCTGCTGGGCGCCCATACACGCTGTGATGATCATCCGGCGCGCTGCCATGGCCA 1458  
Db 6019 TGGGCTCTGCTGGGCGCCCATACACGCTGTGATGATCATCCGGCGCGCTGCCATGGCCA 6078  
QY 1459 CTGCTCTGCTGACTACTGTACGAAACCTCTCTGCTGCTGCTGGGCGCACTCGGCTGT 1518  
Db 6079 CTGCTCTGCTGACTACTGTACGAAACCTCTCTGCTGCTGCTGGGCGCACTCGGCTGT 6138  
QY 1519 GAACCTGTCTCTACCTCTGTGCGACCAACAGCTTCCGCGGGCTTCAACAGCTGCT 1578  
Db 6139 CAACCTGTCTCTACCTCTGTGCGACCAACAGCTTCCGCGGGCTTCAACAGCTGCT 6198  
QY 1579 CTGCCCCAGAGAGCTCAAAATCAGCCCCACAGCTTCCCTGGAGCACTGCTGAAGTGT 1638  
Db 6199 CTGCCCCAGAGAGCTCAAAATCAGCCCCACAGCTTCCCTGGAGCACTGCTGAAGTGT 6258  
QY 1639 GCGCCACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCCCAGGTCTCTGGGCATCTGGC 1698  
Db 6259 GCGCCACAGAGCTCCCTCAGCCAGCGCTCTCTCAGCCCCAGGTCTCTGGGCATCTGGC 6318  
QY 1699 CTGCTGCCCCCTACCGGCTGTCTCCCGAGGGTGAGCCCGCGGTGTCTGTGGCCCT 1758  
Db 6319 CTGCTGCCCCCTACCGGCTGTCTCCCGAGGGTGAGCCCGCGGTGTCTGTGGCCCT 6378  
QY 1759 CTCTTAATGCCACGCGACCCCTGCCATGAGGCGCTTCTGCTGGTGGCGCAGAGGCG 1818  
Db 6379 CTCTTAATGCCACGCGACCCCTGCCATGAGGCGCTTCTGCTGGTGGCGCAGAGGCG 6438  
QY 1819 CCCTCACTGGCTGGAATGAGGCTGGGTGGCGGCGCTCCGCCCCACATCTGGCTCCAC 1878  
Db 6439 CCCTCACTGGCTGGAATGAGGCTGGGTGGCGGCGCTCCGCCCCACATCTGGCTCCAC 6498  
QY 1879 CGGGAGGACAGCTCTGGAGGTCACAGACATGCTGCGCCACCCCTGCTGGTGCCACCTT 1938  
Db 6499 C-GGGAGGACAGCTCTGGAGGTCACAGACATGCTGCGCCACCCCTGCTGGTGCCACCTT 6557  
QY 1939 TCGCAGTTACTGGTTGGTGTCTTCCCAAGCAAGCACTGGGTGTCTCCAGGCTTCT 1998  
Db 6558 TCGCAGTTACTGGTTGGTGTCTTCCCAAGCAAGCACTGGGTGTCTCCAGGCTTCT 6617  
QY 1999 GCGCTAGCAGTTGCTCTGCGAGTCACACACCTGCGACACCCCTGCGACACCTGCGACA 2058  
Db 6618 GCGCTAGCAGTTGCTCTGCGAGTCACACACCTGCGACACCCCTGCGACACCTGCGACA 6677  
QY 2059 CCGTCTCTCTCCCGGACAAAGCCAGGACATGCTGCTTGTGCTGCTCTCTTGGCATA 2118  
Db 6678 CCGTCTCTCTCCCGGACAAAGCCAGGACATGCTGCTTGTGCTGCTCTCTTGGCATA 6737  
QY 2119 AGCCTCAGGCGCTGGCCCTTTCACCCCTCTTCCACCACTCTCTGCGCCCAAAAGTGT 2178  
Db 6738 AGCCTCAGGCGCTGGCCCTTTCACCCCTCTTCCACCACTCTCTGCGCCCAAAAGTGT 6797  
QY 2179 CAAAGGGCCCTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATCTGGGTGTTTTCAGAA 2238  
Db 6798 CAAAGGGCCCTAGGAACCTCGAAGCTGTCTCTGCTTTTCCATCTGGGTGTTTTCAGAA 6857  
QY 2239 AGATGAAGAGAAAAACATGCTGTGAACTTGATGTTGTTGGATGTTTAAATCAAGAGAGA 2298

Db 6858 AGATGAAGAGAAAAACATGCTGTGAACTTGATGTTCTGGGATGTTTAAATCAAGAGAGA 6917  
QY 2299 CAAAATTGCTGAGGAGCTCAGGGCTGGATTGGCAGGTGTGGGCTCCACGCGCTCTCTCC 2358  
Db 6918 CAAAATTGCTGAGGAGCTCAGGGCTGGATTGGCAGGTGTGGGCTCCACGCGCTCTCTCC 6977  
QY 2359 TCCGCTAAGGCTTCCGGCTGAGCTGTGCGAGTGTCTTGCCACCCCGCTCTGGGCTC 2418  
Db 6978 TCCGCTAAGGCTTCCGGCTGAGCTGTGCGAGTGTCTTGCCACCCCGCTCTGGGCTC 7037  
QY 2419 ACACGAGCCCTGGTGGCCAAAGCTGCGCGGCGCACTCTGTTTGTCTCACCCAGGACCTCTG 2478  
Db 7038 ACACGAGCCCTGGTGGCCAAAGCTGCGCGGCGCACTCTGTTTGTCTCACCCAGGACCTCTG 7097  
QY 2479 GGGGTGTTGGAGAGAGGGGCGCGGCTGGGCGCCGAGGGTCCCAAGGCGTGAGGGGCGG 2538  
Db 7098 GGGGTGTTGGAGAGAGGGGCGCGGCTGGGCGCCGAGGGTCCCAAGGCGTGAGGGGCGG 7157  
QY 2539 TCCAGAGAGGTGCGCGGCGAGGGCGCGCTTCCGCCATGTGTGACCCGCTGCCACGGC 2598  
Db 7158 TCCAGAGAGGTGCGCGGCGAGGGCGCGCTTCCGCCATGTGTGACCCGCTGCCACGGC 7217  
QY 2599 CTCTCATGCTCTCTGCTGTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 2658  
Db 7218 CTCTCATGCTCTCTGCTGTGCGGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 7277  
QY 2659 AAGTGTATTTTTTA 2673  
Db 7278 AAGTGTATTTTTTA 7292

## RESULT 8

US-09-891-053-13  
; Sequence 13, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko  
; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yuseke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1893  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (293)...(1209)  
US-09-891-053-13

Query Match 58.9%; Score 1590.2; DB 4; Length 1893;  
Best Local Similarity 98.5%; Pred. No. 1.8e-298;  
Matches 1615; Conservative 0; Mismatches 23; Indels 1; Gaps 1;  
QY 679 CATCAGCTACGACCGCTTCTGCTCGGTGACCCGAGCGGTCTCATACCGGGCCGACGAGG 738  
Db 256 CTTCCGCGCGCGCGCTGACCGCTTCTGCGGTGCTCATACCGGGCCGACGAGG 315





			TYPE: nucleic acid			Query Match		
			STRANDEDNESS: single			Best Local Similarity		
			TOPOLOGY: linear			51.3%; Score 1384.8; DB 3; Length 3244;		
			MOLECULE TYPE: cDNA			Pred. No. 1.2e-258;		
			FEATURE:			Matches 2043; Conservative 0; Mismatches 632; Indels 79; Gaps 20;		
			NAME/KEY: CDS					
			LOCATION: 778..2112					
			US-09-165-543-4					
QY	14	GGCTGACGGTCCGACCGGACGGCTCAGGCTCCGGCTCCTCTCCGCTGAGCAGCG 73						
DB	482	GGGTGACCGACGACCGCGGGCGGTGGAGCT-CGGCTTTGCTCTCGCTGAGCAGCG 540						
QY	74	CGCTGCGGCCCCACTGGGCTGGGA-TCCGGGCCCGGCCCTCGGCACCGCT----- 126						
DB	541	CGCGCGCGCCCACTCCGCTCAGATTCCGACACACAGCCCCCTCTGGATCGGCCCTCTGG 600						
QY	127	-----GCTCTGSCCCCGCGCCCGCGCGGACCATCGCTGGGCGCCCGACGGGAA 180						
DB	601	ACTCTAGCCCGGGCTCTTGCTCCGACCCCGCGACCATGCTCCGGGCGCCCCC-CGAAAA 659						
QY	181	ACCCGACCCGGCCAAAGGCGCCGCAAGACGAGGCTCCCGGGCGGGGCCCCCTCCCGGCG 240						
DB	660	ACCGGGCTGGCGAGAGCGCGCAAGATTAGGCTCACGAGCGGGGCCCCACCCCGGCCA 719						
QY	241	CCGAGTCTCGGCGGGCGGCTTCTCGGACGCTTGACCGGCGGTGAGCTCGGGGGCCAT 300						
DB	720	CCGAGTCTCCGCGCGGTGCGCGGTGTCGCCGAGCGTGTCCCGAGCGGTGTGAGCTGTGGGCCAT 779						
QY	301	GGAGCGCGCGCGCGCGAGCGCGCTGAACTTCGGGGGCGCTGGGCGGAGATCGCGC 360						
DB	780	GGAGCGCGCGCGCGCGAGCGGCTGATGAACGCGTGGGCACTCTGCGCGGAGAGCGCGC 839						
QY	361	GGCGGCGGGCGGGCGGCGGCTTCTCGGACGCTTGACCGGCGGTGCTGGCGCGCTCAT 420						
DB	840	GGCTGACGGCGGGCGGCGGCTTCTCGGCTGCTGGACCGGTGCTCTGGCTGCGCTCAT 899						
QY	421	GGCGTGTCTATGTGGGCCACGGGTGTGGGCAACGGCGTGTGTCATGCTCGCTCTGTGGC 480						
DB	900	GGCGTGTCTATGTGGGCCACGAGTCTGGGCAACGGCGTGTGTCATGCTCGCTCTGTGGC 959						
QY	481	CGACTCGAGCTCCGACCCAGAACAACTTCTTCGTCTCACTCGGCTCATCTCGACTT 540						
DB	960	GGATTGAGGCTCCGACCCAGAACAACTTCTTCGTCTCACTCGGCTCATCTCGACTT 1019						
QY	541	CCTCGTGGCGGCTTCTGATCCCATCTGATGTATGATACCTACGTGCTGACAGGCGCTGGAC 600						
DB	1020	CCTCGTGGGCTTCTGATCCCATCTGATGATGATGATGATGATGATGATGATGATGATGAT 1079						
QY	601	CTTCGGCGGGGCTTCTGACGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 660						
DB	1080	CTTCGGCGGGGCTTCTGACGCTGGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1139						
QY	661	TGCTTTCAACATGCTGCTCATGAGTACGACCGCTTCTGCTGGTACCGGAGCGGCTCTC 720						
DB	1140	GGTCTTTCAACATGCTGCTCATGAGTACGACCGCTTCTGCTGGTACCGGAGCGGCTCTC 1199						
QY	721	ATACCGGGCCAGAGGGTACACGGCGGGCGGAGTGGGAGAGTGGTGGTGGTGGTGGTGGT 780						
DB	1200	CTACAGGGCCAGAGGGGAGACGAGACGGGCGGTTTCGGAAGATGGACTGGTGGTGGT 1259						
QY	781	GCTGGCTTCTGCTGTACGGACCAAGCATCTCGAGCTGGAGTACCTGTCCGGGGGAG 840						
DB	1260	GCTGGCTTCTGCTGTATGGGCTTGCCATCTGAGTTGGAGTACCTGTCTGGTGGCAG 1319						
QY	841	CTCCATCCCGAGGGCCATGCTATGCCGAGTCTTCTACAACTGATCTTCTCATCATCAC 900						
DB	1320	TTCCATCCCGAGGGCCATGCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1379						
QY	901	GGCTTCCACCCCTGGAGTTCTTTTACGCCCTTCTCAGCGTCACTTCTTTAACTCAGCAT 960						
DB	1380	GGCTTCCACCCCTGGAGTTCTTTACGCCCTTCTCAGCGTCACTTCTTTAACTCAGCAT 1439						
QY	961	CTACCTGAACATCCAGAGCGCACCGCTCCGGCTGGATGGGCTCGAGAGCGAGCCG 1020						
DB	1440	CTACCTGAACATCCAGAGCGCACCGCTTCCGGCTGGATGGGCTGGAG---GCTGG 1496						
QY	1021	CCCCGAGCCCTTCCCGAGGCGCCAGCTTCAACACCCCA---CCGCTTGGCTTGGTGGG 1077						
DB	1497	CCAGAAACCCACAGATGCCAGCCCTCGCCACTCCAGCTCCCGGCTGCTGGG 1556						
QY	1078	CTGCTGGCAGAAAGGCGACGGGAGGCGATGCGCTGACAGGTATGGGCTGGTGGAGC 1137						
DB	1557	CTGCTGGCAGAAAGGCGATGCGAGGCGATGCGCTTGCACAGGTATGGGCTGGTGGAGC 1616						
QY	1138	GGCGTAGCGCTGAGGCGGGGAGCGACCTCCGGGGTGGGCTGGGCGGCTCCCT 1197						
DB	1617	AGGCCCTGGTGTGAGGCTGGGGAGGCTGCTCCGGGGTGGAGTGGAGGTGCTGC 1676						
QY	1198	GGCTTCCACCCCTCCAGCTCCGGGAGCTTCTCGAGGGGCACTGAGAGCGCGCTCACT 1257						
DB	1677	TGCTCGCCCACTCCAGCTCTGGCAGCTCTCTCAAGGGGCACTGAGAGGCCAGCTCACT 1736						
QY	1258	CAAGAGGGGCTCCAAAGCGTCCGCTCGGCTCGCTGGAGAGCGCATGAAGATGGT 1317						
DB	1737	CAAAAGGGGCTCCAAAGCGATCAGCATCTTTCAGCATCTCTGGAGAGCGCATGAAGATGGT 1796						
QY	1318	GTCCAGAGCTTCCAGCGGCTTTCGGCTGTCTCGGGACAGAAAGTGGCCAAAGTCGCT 1377						
DB	1797	GTCCAGAGCATCACCCAGCGCTTCCGGCTGTCTGGGGCAAGAGGTGGCCAAAGTCGCT 1856						
QY	1378	GGCGCTCATCGTGAGCATCTTTGGGCTGTCTGGGCGCCCATACAGCTCTCTGATGATCAT 1437						
DB	1857	GGCATCATCGTGAGCATCTTTGGGCTGTCTGGGCGCGGTACACGCTCTCTTAATGATCAT 1916						
QY	1438	CGGGCGCGCTGCCATGGCCACTGCGTCCCTGACTACTGGTACGAAACCTCTCTTGGCT 1497						
DB	1917	CGAGCTGCTTGGCATGGCGCTGATCCCGCTCTCTACCCACTGTGGCACTCAGACTTCCG 1976						
QY	1498	CCTGTGGGCAACTCGGCTGTCAACCTGTCTCTACCTCTGTGCCACACAGCTTCCG 1557						
DB	1977	TCTGTGGGCAACTCGGCGGTCAACCCGCTCTCTACCCACTGTGGCACTCAGACTTCCG 2036						
QY	1558	CGGGCTTCCAAAGCTGTCTGCGCCCGAGAGCTCAAAATCCAGCCCGCCACAGCTCCCT 1617						
DB	2037	CAGAGCTTCCAAAGCTGTCTGCGCCCGAGAGCTCAAGTTCAGGCTCCAGCCCGCTCCCT 2096						
QY	1618	GGAGCACTGCTGGAAAGTGGGCGCCACAGAGCTTCCCTCAGCCACGCTCTCTCAGCC 1677						
DB	2097	GGAGCACTGCTGGAAAGTGGAGCAG-CTGCGCCACCTTCTGAGGCGCAGGCTTGTACTTG 2155						
QY	1678	CAGGTCTCTGGGCTGTGGGCTGTGCGGCTTACCGGCTCGTTCGCCAGGGGTGAG 1737						
DB	2156	TTTGAGTGGGCGAGCGGAGCGTGGGCGGGGCTTCCATGCTCCGCTCCAAATGCCAT 2215						
QY	1738	CCCGGCTGTCTGTGGGCTCTCTTAATG-----CCAGCGGAGCCACCTT 1783						
DB	2216	GGCGGCTCTTAGATCATCAACCCCGAGTGGGGTAGCATGGCAGGTGGGCGCAGAGCCC 2275						
QY	1784	GCCATGGAGGGGCTTCTCGGTTGGCCAGAGGGGCTTCTACTGGCT-GGACTGGAGGT 1842						
DB	2276	TAGTTGGTGGAGCTAGAGTGTCTGTTAGCTCTGCCGCGCATCTCTCTTCCACACACA 2335						
QY	1843	GGGTGGCGGCGCTTCCGCCCCACATCTGGCTTCCACGGGGAGGAGCAGTCTGGAGGTCC 1902						
DB	2336	GAAGAGACAAATCCAGGAGTCCAGGCTTCCAGCTTCCACCTTACACACACACACACA 2395						
QY	1903	CAGACATGCGCCAC-----CCCTGTGTGTCGCCACCTTGCAGTTACTGTTGG 1955						
DB	2396	CACACACACACACACAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGT 2455						
QY	1956	TGTTCTTCCAAAGACACCTGGGTGTGTCTCCAGGCTTCTCTGCC-----CT 2003						

```
Db 2456 TGTCTCCCTTAATGCAAACTCGGTGTGTCTCCGGCTCCGGCTCGCAATGCGTGG 2515
QY 2004 AGCAGTTTCCCTCTGACGTGACACACCTGACACACCTGACACACCTGACACCGTTC 2063
Db 2516 TGGCCCTGCTATGTGTCAACCGCCACACACCGCCGCGCCACACACTTGCACACCTTC 2575
QY 2064 CCTCTCCCGGACAAAGCCACAGACACTGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2123
Db 2576 CTCTCTCCAGAGAGCTGGGAGAGAGTCCCTTTGCTGCACTGCTCTGCTTAAATCCC 2635
QY 2124 CAGGCTGCGCTTTTCAACCCCTCTTCCCAACCACTCTCTGCTGCCCCCAAAAGTGTCAAGG 2183
Db 2636 AGAGCTGCTCTTATATCCCCACCTCTCCCTTCAA--CTCTGCCCAACAAAGTGTGAGC 2693
QY 2184 GGCCTTAGAACTCGAAGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2242
Db 2694 GCTCGGGAACCTTGAAGCTTCTGCTCTCC--TTCCACTCTGATGTTTTCAGGAAGATG 2751
QY 2243 --GAAGAGAAACATGCTGTGAACCTGATGCTGCTGGGATGTTTAAATCAAGAGAGACA 2300
Db 2752 GAGGAGAAACACAGCTGTGAACCTTGATGTTCTTGGATGTTTAAATCAAGAGAGACA 2811
QY 2301 AAATTGCTGAGAGCTCAGGCTGGAATGGCAGGTGTGGGCTCCCAAGCCCTCTCTCCCTC 2360
Db 2812 AAATTGCCAGAGCTCGGGCTGGATTGGCAGGTGTGGGCTCCCAAGCCCTCTCTCCCTC 2871
QY 2361 --CGCTAAGCTTCGGCTGAGCTGTCAGCTGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCG 2417
Db 2872 AGTGTGTCAGCTTCGGCTGAGCGCGCAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 2931
QY 2418 --CACACACAGCCTGTGTGCGAAGCTGCTGCGGCGCAGCTGCTGCTGCTGCTGCTGCTGCT 2475
Db 2932 GGGACATGCGCCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2991
QY 2476 CTGGGGTGTGTTGGG---AGGAGGGGGCCCGGCTGGGCGCGAGGGTCCCAAGGCGTGCAG 2532
Db 2992 TATGGGTAGAGCGGCTCTTCACTGTGCTTAAAGTCTTGAAGTCTCAGGCTCAGGACAGTCA 3051
QY 2533 GGGCGG----TCAGAGAGGTGCCCGGCGAGGGCGGCTTCCGCAATGCTGTGTGACCC 2588
Db 3052 CAGGAGAGCAGGCGGCGCGACACTGGGAGGAATGCTTGGCTGCTGCTGCTGCTGCTGCTGCT 3111
QY 2589 GTGCCACGCTCTGATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2645
Db 3112 ACCTAGGC--TTCTGATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3170
QY 2646 TGAGGTCAACAATAAGTGTATTTTTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2699
Db 3171 TGAAGACAAATAAGTGTATTTTTTAAAAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3224
```

## RESULT 10

US-09-891-053-21

; Sequence 21, Application US/09891053

; Patent No. 6750322

; GENERAL INFORMATION:

; APPLICANT: Itadani, Hiraku

; APPLICANT: Takimura, Tetsuo

; APPLICANT: Nakamura, Takao

; APPLICANT: Kobayashi, Masahiko

; APPLICANT: Tanaka, Ken-ichi

; APPLICANT: Hidaka, Yusuke

; APPLICANT: Ohta, Masataka

; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

; FILE REFERENCE: 06501-083001

; CURRENT APPLICATION NUMBER: US/09/891,053

; PRIOR FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: PCT/JP99/07280

; PRIOR FILING DATE: 1999-12-24

; PRIOR APPLICATION NUMBER: PCT/JP98/05967

; PRIOR FILING DATE: 1998-12-25

```
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 2050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (271)...(1629)
US-09-891-053-21
```

Query Match 50.4%; Score 1360.4; DB 4; Length 2050;

Best Local Similarity 99.9%; Pred. No. 5.5e-254;

Matches 1361; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 271 TCCCGAGCCGCGTGTGAGCTGTGGGGCCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330
Db 243 TCCCGAGCCGCGTGTGAGCTGTGGGGCCATGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 302
QY 331 CGTTTCGGGGCGCTGTGGCGGCGATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 390
Db 303 CGTTTCGGGGCGCTGTGGCGGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 362
QY 391 AGCCTGGACCGCGGTGCTGGCGCGCTCATATGGCGCTGCTCATATGGCGCGCGCGCGCGCGCGCG 450
Db 363 AGCCTGGACCGCGGTGCTGGCGCGCTCATATGGCGCTGCTCATATGGCGCGCGCGCGCGCGCGCG 422
QY 451 CAACCGCTGTGTCTATGCTGTGCGCTTCTGTCGCGCGCTTCGAGAGCTTCGCGACCCAGAACTTT 510
Db 423 CAACCGCTGTGTCTATGCTGTGCGCTTCTGTCGCGCGCTTCGAGAGCTTCGCGACCCAGAACTTT 482
QY 511 CTTCCTGTCTAACTTCGCGCATCTCCGACTTCTCTGTGGCGCGCTTCTGATCCCACTGTA 570
Db 483 CTTCCTGTCTAACTTCGCGCATCTCCGACTTCTCTGTGGCGCGCTTCTGATCCCACTGTA 542
QY 571 TGTACCTTACCTGTGTGACAGCGCGCTGACCTTGTGGCGCGCGCGCGCTTCTCAAGCTGTGGCT 630
Db 543 TGTACCTTACCTGTGTGACAGCGCGCTTGTGACCTTGTGGCGCGCGCGCGCTTCTCAAGCTGTGGCT 602
QY 631 GGTAGTGAGTACCTGTGTGTGACCTTCTCTGCTTCAACATCTGTGCTCATCAGTACGA 690
Db 603 GGTAGTGAGTACCTGTGTGTGACCTTCTCTGCTTCAACATCTGTGCTCATCAGTACGA 662
QY 691 CGCTTCTGTGCTGTCACCGAGCGGTCTCATACCGGCGCGAGCGGTGACACCGCGCG 750
Db 663 CGCTTCTGTGCTGTCACCGAGCGGTCTCATACCGGCGCGAGCGGTGACACCGCGCG 722
QY 751 GGCAGTGGGAGAGTGTGTGTGGTGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 810
Db 723 GGCAGTGGGAGAGTGTGTGTGGTGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 782
QY 811 CTGAGCTGGGAGTACCTGTTCGGGGCGAGTTCATCCCGAGGGCCACTGCTATGCCGA 870
Db 783 CTGAGCTGGGAGTACCTGTTCGGGGCGAGTTCATCCCGAGGGCCACTGCTATGCCGA 842
QY 871 GTTCTTTTAACTGTGTTCTTCTCATACGGCTTTCACCTTGGAGTTCCTTTACGCCCTT 930
Db 843 GTTCTTTTAACTGTGTTCTTCTCATACGGCTTTCACCTTGGAGTTCCTTTACGCCCTT 902
QY 931 CCTCAGCTCACCTTCTTTTAACTTACCTCAGCATCTACCTGAACATCCAGAGCGGCACCGGCT 990
Db 903 CCTCAGCTCACCTTCTTTTAACTTACCTCAGCATCTACCTGAACATCCAGAGCGGCACCGGCT 962
QY 991 CCGGCTGGATGGGCTCGAGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 1050
Db 963 CCGGCTGGATGGGCTCGAGAGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTC 1022
QY 1051 ACCACCCCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1110
Db 1023 ACCACCCCAACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1082
```

1111	Qy	GCTCCACAGGTA	TATGGGTGGGT	GAGCGGCCG	CTGATGGCGCT	GAGCCCGGGG	GAGCGAC	CCCT	1170
1083	Db	GCTCCACAGGTA	TATGGGTGGGT	GAGCGGCCG	CTGATGGCGCT	GAGCCCGGGG	GAGCGAC	CCCT	1142
1171	Qy	CGGGGTGGGGT	GCGGGCGGCT	CCGTGGCTT	CACCACTT	CACAGCTC	CGCGAGCT	CCTC	1230
1143	Db	CGGGGTGGGGT	GCGGGCGGCT	CCGTGGCTT	CACCACTT	CACAGCTC	CGCGAGCT	CCTC	1202
1231	Qy	GAGGGGCACT	GAGAGCGCGCT	CAC	TCAAGAGGGCT	CCAGCCGT	GCGGCTCCT	CGGC	1290
1203	Db	GAGGGGCACT	GAGAGCGCGCT	CAC	TCAAGAGGGCT	CCAGCCGT	GCGGCTCCT	CGGC	1262
1291	Qy	CTCGCTGGAGA	AGCGCATGAAG	TGGTGT	CCAGAGCTT	CAC	CAGCGCTT	TGGGCTGT	1350
1263	Db	CTCGCTGGAGA	AGCGCATGAAG	TGGTGT	CCAGAGCTT	CAC	CAGCGCTT	TGGGCTGT	1322
1351	Qy	TCGGGACAGGAA	AGTGCGCAAGT	CGCTGGCGCT	CATCGTGAGCAT	TTTGGGCT	TGCTGT	1410	
1323	Db	TCGGGACAGGAA	AGTGCGCAAGT	CGCTGGCGCT	CATCGTGAGCAT	TTTGGGCT	TGCTGT	1382	
1411	Qy	GGCCCCATAC	ACGCTGTGAT	GATCAT	CCGGGCGCGCT	GCCATGGCCAC	TGCGTCCCTGA	1470	
1383	Db	GGCCCCATAC	ACGCTGTGAT	GATCAT	CCGGGCGCGCT	GCCATGGCCAC	TGCGTCCCTGA	1442	
1471	Qy	CTACTGTGA	CGAAACCT	CTCTTGGCT	CTCTGTGGGCCAA	CTCGGCTGT	CAACCCCTGT	1530	
1443	Db	CTACTGTGA	CGAAACCT	CTCTTGGCT	CTCTGTGGGCCAA	CTCGGCTGT	CAACCCCTGT	1502	
1531	Qy	CTACCTCTGT	GCCACACAGCT	CTCCGCGGCGCT	TCCACCAAGTGCT	CTGCCCCGAA		1590	
1503	Db	CTACCTCTGT	GCCACACAGCT	CTCCGCGGCGCT	TCCACCAAGTGCT	CTGCCCCGAA		1562	
1591	Qy	GCTCAAAAT	CCAGCCCCAC	AGCTCCCT	CTGGAGCA	TGCTGGAA		1632	
1563	Db	GCTCAAAAT	CCAGCCCCAC	AGCTCCCT	CTGGAGCA	TGCTGGAA		1604	

```

RESULT 11
US-09-167-354-6
; Sequence 6, Application US/09167354A
; Patent No. 6136559
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; TITLE OF INVENTION: SUBTYPE
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/167,354A
; CURRENT FILING DATE: 1998-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDNA
US-09-167-354-6

Query Match          49.5%; Score 1335; DB 3; Length 1335;
Best Local Similarity 100.0%; Pred. No. 4.1e-249;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      299  ATGGAGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGAGCGCTTTCCGGGGGGCGCTGGCGGGCGATGCG 358
          |||||
Db       1  ATGAGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGAGCGCTTTCCGGGGGGCGCTGGCGGGCGATGCG 60

Qy      359  GCGGCGCGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGAGCGCGCTTGGCGGGCGCGCTC 418
          |||||
Db       61  GCGGCGCGCGCGCGCGCGCGCGCGCTTCTCGGCGAGCTTGGAGCGCGCTTGGCGGGCGCGCTC 120

```

Qy	419	ATGCGCTGCTCATGCTGGGCCACGGTGTCTGGGCAACGGCTGTGTCACTGCTCGCTTTCGTG	478
Db	121	ATGCGCTGCTCATGCTGGGCCACGGTGTCTGGGCAACGGCTGTGTCACTGCTCGCTTTCGTG	180
Qy	479	GCGACTCGAGCCTCCGACCCAGAAACAATTCTTCTGCTCAACTCGGCATCTCCGAC	538
Db	181	GCGACTCGAGCCTTCGACCCAGAAACAATTCTTCTGCTCAACTCGGCATCTCCGAC	240
Qy	539	TTCTCTCGTCCGGCGCTTCTGTCATCCCACTGTATGTATACCTTACGTGTGTGACAGGCCGTGG	598
Db	241	TTCTCTCGTCCGGCGCTTCTGTCATCCCACTGTATGTATACCTTACGTGTGTGACAGGCCGTGG	300
Qy	599	ACCTTCCGGCCGGGGCTCTCTCAAGCTGTGGCTGGTAGTGGACATACCTGCTGTGTGCACCTCC	658
Db	301	ACCTTCCGGCCGGGGCTCTCTCAAGCTGTGGCTGGTAGTGGACATACCTGCTGTGTGCACCTCC	360
Qy	659	TCTGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGGTCAACCGAGCGGTC	718
Db	361	TCTGCCTTCAACATCGTGTCTCATCAGCTACGACCGCTTCTGTGCGGTCAACCGAGCGGTC	420
Qy	719	TCATACCGGGCCACGAGGGTGTACACGCGCGGGCCAGTGTGGAAAGATGTCTGTGTGTGG	778
Db	421	TCATACCGGGCCACGAGGGTGTACACGCGCGGGCCAGTGTGGAAAGATGTCTGTGTGTGG	480
Qy	779	GTGCTGCCCTTCTGTCTGTATCGGACGAGCCATCTCTGAGCTGGAGTAGCTGTCCGGGGCC	838
Db	481	GTGCTGCCCTTCTGTGTATCGGACGAGCCATCTCTGAGCTGGAGTAGCTGTCCGGGGCC	540
Qy	839	AGCTTCCATCCCGAGGGCCATGCTATGCGAGTCTTCTTACAACTGGTACTTCCTCATC	898
Db	541	AGCTTCCATCCCGAGGGCCATGCTATGCGAGTCTTCTTACAACTGGTACTTCCTCATC	600
Qy	899	ACGGCTTCCACCTGGAGTCTTTTACGCCCTTCTCTCAGCGTCACTTCTTTTAACCTCAGC	958
Db	601	ACGGCTTCCACCTGGAGTCTTTTACGCCCTTCTCTCAGCGTCACTTCTTTTAACCTCAGC	660
Qy	959	ATCTACTGAACATCCAGAGGCGCACCCGCTCCGCTGTGATGGGCTCGAGAGGCAGCC	1018
Db	661	ATCTACTGAACATCCAGAGGCGCACCCGCTCCGCTGTGATGGGCTCGAGAGGCAGCC	720
Qy	1019	GGCCCCGAGCCCCCTCCGAGGGCCAGCCCTCACACCCCCACCCTGGCTGTGGGCTGGGGC	1078
Db	721	GGCCCCGAGCCCCCTCCGAGGGCCAGCCCTCACACCCCCACCCTGGCTGTGGGCTGGGGC	780
Qy	1079	TGCTGGCAGAAAGGGCAGCGGGAGGCGCATGCCCTGCACAGGTTATGGGTGGGTGAGGCG	1138
Db	781	TGCTGGCAGAAAGGGCAGCGGGAGGCGCATGCCCTGCACAGGTTATGGGTGGGTGAGGCG	840
Qy	1139	GCCGTAGGCGCTCAGGCCCCGGGAGGCGACCTCTCGGGGTGGCGGTGGGGCGGCTCCGTG	1198
Db	841	GCCGTAGGCGCTCAGGCCCCGGGAGGCGACCTCTCGGGGTGGCGGTGGGGCGGCTCCGTG	900
Qy	1199	GCTTCACCCACCTCCAGCTCCGCGAGCTCTCTGAGGGGCACCTGAGAGGGCGGCTCCTCT	1258
Db	901	GCTTCACCCACCTCCAGCTCCGCGAGCTCTCTGAGGGGCACCTGAGAGGGCGGCTCCTCT	960
Qy	1259	AAGAGGGCTTCCAAGCCGTCCGGCTCTCTGGCTCTGAGAGAGCGCATGAAGATGGTG	1318
Db	961	AAGAGGGCTTCCAAGCCGTCCGGCTCTCTGGCTCTGAGAGAGCGCATGAAGATGGTG	1020
Qy	1319	TCCAGAGCTTCAACGAGCTTTTCGGCTGTCTCGGACAGGAAAGTGCCCAAGTCGCTG	1378
Db	1021	TCCAGAGCTTCAACGAGCTTTTCGGCTGTCTCGGACAGGAAAGTGCCCAAGTCGCTG	1080
Qy	1379	GCGTCAATCGTAGCATCTTTTGGGCTCTGCTGGGCCCCCATACACGCTGCTGATGATCATC	1438
Db	1081	GCGTCAATCGTAGCATCTTTTGGGCTCTGCTGGGCCCCCATACACGCTGCTGATGATCATC	1140
Qy	1439	CGGGCCGCTGCCATGGCCACATGCGTCCCTGACTACTGTGTAGAAACCTCTTCTGGCTC	1498
Db	1141	CGGGCCGCTGCCATGGCCACATGCGTCCCTGACTACTGTGTAGAAACCTCTTCTGGCTC	1200
Qy	1499	CTGTGGGCCAACTCGGCTGTCAACCCCTGTCTCTACCTCTCTGTGCCACACAGCTTCCGC	1558

```
Db 1201 CTGTGGCCAACTCGGCTGCAACCTGTCTTACCTCTGTGCGCCACACAGCTTCGCG 1260
QY 1559 CGGGCTTCCACCAAGTGTCTGTGCCCCCAGAAAGCTCAAAATCAGCCCCACAGTCCCTG 1618
Db 1261 CGGGCTTCCACCAAGTGTCTGTGCCCCCAGAAAGCTCAAAATCAGCCCCACAGTCCCTG 1320
QY 1619 GAGCACTGCTGGAAG 1633
Db 1321 GAGCACTGCTGGAAG 1335

RESULT 12
US-09-642-855-6
; Sequence 6, Application US/09642855
; Patent No. 6413743
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Erlander, Mark
; APPLICANT: Pyati, Jayashree
; APPLICANT: Huvar, Arne
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3
; FILE REFERENCE: JMW
; CURRENT APPLICATION NUMBER: US/09/642,855
; CURRENT FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: 09/167,354
; PRIOR FILING DATE: 1998-10-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDNA
US-09-642-855-6

Query Match 49.5%; Score 1335; DB 3; Length 1335;
Best Local Similarity 100.0%; Pred. No. 4.1e-249;
Matches 1335; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 299 ATGGAGCGCGCGCGCGCGCGCGCGCTGAAAGCTTGGGGGGCGTGGCGGGCGATGCG 358
Db 1 ATGGAGCGCGCGCGCGCGCGCGCGCTGAAAGCTTGGGGGGCGTGGCGGGCGATGCG 60
QY 359 GCGGCGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGGACCGCGTGTGCGCGCGCTC 418
Db 61 GCGGCGCGCGCGCGCGCGCGCGCTTCTCGGAGCGCTGGACCGCGTGTGCGCGCGCTC 120
QY 419 ATGGCGCTGCTCATGCTGGCCAGGCTGTGGGGAACGCGCTGTGATGCTGCGCTTGGTG 478
Db 121 ATGGCGCTGCTCATGCTGGCCAGGCTGTGGGGAACGCGCTGTGATGCTGCGCTTGGTG 180
QY 479 GCGGACTCGAGCTCGCGACCCAGAACAACTTCTTCTGCTCAACTCGGCTGCAATCCGAC 538
Db 181 GCGGACTCGAGCTCGCGACCCAGAACAACTTCTTCTGCTCAACTCGGCTGCAATCCGAC 240
QY 539 TTCTCTGTCGGCGCTTCTGCTATCCACATGTATGATACCTTGTGATGCTGACGCGCGTGG 598
Db 241 TTCTCTGTCGGCGCTTCTGCTATCCACATGTATGATACCTTGTGATGCTGACGCGCGTGG 300
QY 599 ACCTTCGCGCGCGCTTCTGCAAGCTGTGGTGTGAGTGAATCTGCTGTGCACTTCC 658
Db 301 ACCTTCGCGCGCGCTTCTGCAAGCTGTGGTGTGAGTGAATCTGCTGTGCACTTCC 360
QY 659 TCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTGCTGCTGCACTGCGGCTG 718
Db 361 TCTGCTTCAACATCGTGTCTCATAGTACGACCGCTTCTGCTGCTGCACTGCGGCTG 420
QY 719 TCATACCGGGCCAGCAGGGGTGACACGCGCGGGGAGATGCTGCTGCTGCTG 778
Db 421 TCATACCGGGCCAGCAGGGGTGACACGCGCGGGGAGATGCTGCTGCTGCTG 480
```

## RESULT 13

US-09-642-514-6

; Sequence 6, Application US/09642514

; Patent No. 6437100

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; TYPE OF INVENTION: SUBTYPE

```
QY 779 GTGCTGGCTTCTCTGTACGGACCAAGCCATCTGTAGCTGGAGTACTGTTCGGGGGCG 838
Db 481 GTGCTGGCTTCTCTGTGTACGGACCAAGCCATCTGTAGCTGGAGTACTGTTCGGGGGCG 540
QY 839 AGCTTCATCCCGAGGGGCACTGTGTATCCCGAGTCTTCTTACAACTGGTACTTCTCTCATC 898
Db 541 AGCTTCATCCCGAGGGGCACTGTGTATCCCGAGTCTTCTTACAACTGGTACTTCTCTCATC 600
QY 899 ACGGCTTCCACCTGGAGTCTTGTACGCCCTTCTTACGCCCTTCTTACGCCCTTCTTAACTCAGC 958
Db 601 ACGGCTTCCACCTGGAGTCTTGTACGCCCTTCTTACGCCCTTCTTACGCCCTTCTTAACTCAGC 660
QY 959 ATCTACCTGAACATCCAGAGGGCGACCCGCTCGGGCTGGATGGGCTCGAGAGGACGCC 1018
Db 661 ATCTACCTGAACATCCAGAGGGCGACCCGCTCGGGCTGGATGGGCTCGAGAGGACGCC 720
QY 1019 GGGCCGAGCGCCCTCCCGAGGGCCAGCCCTCACACCCCCACCCCTTGGCTGTGGGCG 1078
Db 721 GGGCCGAGCGCCCTCCCGAGGGCCAGCCCTCACACCCCCACCCCTTGGCTGTGGGCG 780
QY 1079 TGCTGGCAGAAAGGGGCACGGGGAGGCCATGCGCTGTGCAAGGTATGGGGTGGGTGAGGCG 1138
Db 781 TGCTGGCAGAAAGGGGCACGGGGAGGCCATGCGCTGTGCAAGGTATGGGGTGGGTGAGGCG 840
QY 1139 GCCGTAGGCGCTGAGGCGGGGAGCGACCCCTCGGGGTGGGCTGGGGGGCGCTCCGCTG 1198
Db 841 GCCGTAGGCGCTGAGGCGGGGAGCGACCCCTCGGGGTGGGCTGGGGGGCGCTCCGCTG 900
QY 1199 GCTTCACCCACCTCCAGCTCCGGGAGCTTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 1258
Db 901 GCTTCACCCACCTCCAGCTCCGGGAGCTTCTCGAGGGGCACTGAGAGGCGCGCTCACTC 960
QY 1259 AAGAGGGGCTCAAGCCCTCGGCGCTTCTCGGCTCGCTGGAGAGCGCATGAAGATGGTG 1318
Db 961 AAGAGGGGCTCAAGCCCTCGGCGCTTCTCGGCTCGCTGGAGAGCGCATGAAGATGGTG 1020
QY 1319 TCCAGAGCTTCAAGCCAGGCTTTCGGCTGTCTGGGACAGAAAGTGGCAAGTCCGCTG 1378
Db 1021 TCCAGAGCTTCAAGCCAGGCTTTCGGCTGTCTGGGACAGAAAGTGGCAAGTCCGCTG 1080
QY 1379 GCGGCTCATGAGCATCTTTGGGCTTGTGCGGCCCATACACGCTGCTGATGATCATC 1438
Db 1081 GCGGCTCATGAGCATCTTTGGGCTTGTGCGGCCCATACACGCTGCTGATGATCATC 1140
QY 1439 CGGGCGCTGCTGCATGCGCACTGCGTCCCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1498
Db 1141 CGGGCGCTGCTGCATGCGCACTGCGTCCCTGACTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY 1499 CTGTGGGCAACTCGGCTGCAACCTGTCTCTACCTGTGTGCGCACACAGCTTCGCG 1558
Db 1201 CTGTGGGCAACTCGGCTGCAACCTGTCTCTACCTGTGTGCGCACACAGCTTCGCG 1260
QY 1559 CGGGCTTTCACCAAGCTGCTTGTGCGGCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1618
Db 1261 CGGGCTTTCACCAAGCTGCTTGTGCGGCCAGAGCTCAAAATCCAGCCCCACAGCTCCCTG 1320
QY 1619 GAGCACTGCTGGAAG 1633
Db 1321 GAGCACTGCTGGAAG 1335
```

## RESULT 13

US-09-642-514-6

; Sequence 6, Application US/09642514

; Patent No. 6437100

; GENERAL INFORMATION:

; APPLICANT: Lovenberg, Timothy

; APPLICANT: Erlander, Mark

; APPLICANT: Pyati, Jayashree

; APPLICANT: Huvar, Arne

; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3

; TYPE OF INVENTION: SUBTYPE











**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 2, 2005, 19:57:02 ; Search time 27 Seconds  
(without alignments)  
1230.327 Million cell updates/sec

Title: US-10-727-021-7  
Perfect score: 2361  
Sequence: 1 MERAPPDGLNAGALAGDA.....LLCPQKLIKPHSSLEHCWK 445

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues  
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2361	100.0	445	3	US-09-167-354-7
2	2361	100.0	445	4	US-09-642-855-7
3	2361	100.0	445	4	US-09-642-514-7
4	2357	99.8	445	2	US-08-985-090-2
5	2357	99.8	445	3	US-09-165-543-2
6	2357	99.8	449	4	US-09-949-016-10930
7	2357	99.8	453	4	US-09-891-053-20
8	2213	93.7	445	3	US-09-165-543-5
9	2213	93.7	445	4	US-09-891-053-25
10	2057	87.1	413	4	US-09-891-053-1
11	1828	77.4	362	2	US-08-985-090-5
12	1828	77.4	362	3	US-09-165-543-32
13	1820	77.1	351	3	US-09-524-162-2
14	724	30.7	390	3	US-09-812-010-2
15	724	30.7	390	4	US-09-812-216-2
16	598.5	25.3	479	1	US-08-313-553-7
17	598.5	25.3	479	3	US-08-767-993-7
18	584.5	24.8	460	4	US-09-826-509-513
19	541	22.9	590	4	US-09-538-092-967
20	540	22.9	355	1	US-08-118-270-11
21	540	22.9	355	5	PCT-US93-08528-11
22	536	22.7	590	4	US-09-826-509-517
23	535	22.7	479	4	US-09-826-509-519
24	527.5	22.3	532	4	US-09-826-509-521
25	527	22.3	348	1	US-08-118-270-13
26	527	22.3	348	5	PCT-US93-08528-13
27	523	22.2	342	1	US-08-118-270-9

28	523	22.2	342	5	PCT-US93-08528-9	Sequence 9, Appli
29	516.5	21.9	466	4	US-09-826-509-515	Sequence 515, App
30	516	21.9	354	1	US-08-313-553-9	Sequence 9, Appli
31	516	21.9	354	3	US-08-767-993-9	Sequence 9, Appli
32	515.5	21.8	466	1	US-08-194-338-11	Sequence 11, Appli
33	498.5	21.1	601	1	US-07-676-174A-2	Sequence 2, Appli
34	496.5	21.0	461	1	US-08-194-338-4	Sequence 4, Appli
35	477.5	20.2	450	1	US-08-444-734A-8	Sequence 8, Appli
36	477	20.2	450	4	US-09-825-923-2	Sequence 2, Appli
37	474.5	20.1	447	4	US-09-825-923-2	Sequence 2, Appli
38	474	20.1	333	5	US-08-118-270-12	Sequence 12, Appli
39	474	20.1	333	5	PCT-US93-08528-12	Sequence 12, Appli
40	468.5	19.8	450	1	US-08-194-338-5	Sequence 5, Appli
41	465.5	19.7	601	1	US-08-194-338-2	Sequence 2, Appli
42	458.5	19.4	472	1	US-08-194-338-6	Sequence 6, Appli
43	452	19.1	468	2	US-08-390-000A-7	Sequence 7, Appli
44	452	19.1	477	1	US-08-087-772A-16	Sequence 16, Appli
45	446	18.9	477	1	US-08-444-734A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-167-354-7  
; Sequence 7, Application US/09167354A  
; Patent No. 6136559  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; TITLE OF INVENTION: SUBTYPE  
; FILE REFERENCE: JMW  
; CURRENT APPLICATION NUMBER: US/09/167,354A  
; CURRENT FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-167-354-7

Query Match	100.0%;	Score 2361;	DB 3;	Length 445;
Best Local Similarity	100.0%;	Pred. No. 3.7e-161;		
Matches 445;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MERAPPDGLNAGALAGDAAGGARGFSAAWTAVLAALMALLIVATVGLGNALVLA	60	
Db	1	MERAPPDGLNAGALAGDAAGGARGFSAAWTAVLAALMALLIVATVGLGNALVLA	60	
Qy	61	ADSSLRQNNFLLNLALSDFLVGAFCIPLYVPYVLTGRTWTFGRGLCKLWLVVDLLCTS	120	
Db	61	ADSSLRQNNFLLNLALSDFLVGAFCIPLYVPYVLTGRTWTFGRGLCKLWLVVDLLCTS	120	
Qy	121	SAFNIVLSYDRFVSUTRAVSRAQQGTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180	
Db	121	SAFNIVLSYDRFVSUTRAVSRAQQGTRRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180	
Qy	181	SSIPGHCYAEFFNNWYFLITASTLEFPTPLSVTFNNLSIYLNIOFTRLRLDCAREAA	240	
Db	181	SSIPGHCYAEFFNNWYFLITASTLEFPTPLSVTFNNLSIYLNIOFTRLRLDCAREAA	240	
Qy	241	GPEPPEAQPPPPPPGCGWQKGHGAMPLHRYGVGEAAVGAAGATLGGGGGGSV	300	
Db	241	GPEPPEAQPPPPPPGCGWQKGHGAMPLHRYGVGEAAVGAAGATLGGGGGGSV	300	
Qy	301	ASPTSSSGSSRGTERPRSLKRGSKPSASSASLEKRMKVQSQSFQTRFLSDRDKVAKSL	360	

Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQFTQRFSLSDRKVAKSL 360  
QY 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTSTFWLLWANSVAVNPVLPCHHSFR 420  
Db 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTSTFWLLWANSVAVNPVLPCHHSFR 420  
QY 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445  
Db 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445

## RESULT 2

US-09-642-855-7  
; Sequence 7, Application US/09642855  
; Patent No. 6413743  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,855  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: 09/167,354  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-642-855-7

Query Match 100.0%; Score 2361; DB 4; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.7e-161;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVGLNGLVLAFLV 60  
Db 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVGLNGLVLAFLV 60  
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFCLPYVPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
Db 61 ADSSLRTQNNFLLNLAIISDFLVGAFCLPYVPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
QY 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
Db 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNQRTLRDLDCAREAA 240  
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNQRTLRDLDCAREAA 240  
QY 241 GPEPPEAQSPPPPPGCGCWKGHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
Db 241 GPEPPEAQSPPPPPGCGCWKGHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
QY 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQFTQRFSLSDRKVAKSL 360  
Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQFTQRFSLSDRKVAKSL 360  
QY 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTSTFWLLWANSVAVNPVLPCHHSFR 420  
Db 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTSTFWLLWANSVAVNPVLPCHHSFR 420  
QY 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445  
Db 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445

## RESULT 3

US-09-642-514-7  
; Sequence 7, Application US/09642514  
; Patent No. 6437100  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Erlander, Mark  
; APPLICANT: Pyati, Jayashree  
; APPLICANT: Huvar, Arne  
; TITLE OF INVENTION: DNA ENCODING A HUMAN HISTAMINE RECEPTOR OF THE H3  
; FILE REFERENCE: SUBTYPE  
; CURRENT APPLICATION NUMBER: US/09/642,514  
; PRIOR FILING DATE: 2000-08-21  
; PRIOR APPLICATION NUMBER: US 09/167,354  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 445  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:PEPTIDE  
US-09-642-514-7

Query Match 100.0%; Score 2361; DB 4; Length 445;  
Best Local Similarity 100.0%; Pred. No. 3.7e-161;  
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVGLNGLVLAFLV 60  
Db 1 MERAPDGLNAGSALAGDAAAAGARGFSAATVLAALMALLIVATVGLNGLVLAFLV 60  
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFCLPYVPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
Db 61 ADSSLRTQNNFLLNLAIISDFLVGAFCLPYVPVYLTGRWTFGRGLCKLWLVVDYLLCTS 120  
QY 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
Db 121 SAFNVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNQRTLRDLDCAREAA 240  
Db 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNQRTLRDLDCAREAA 240  
QY 241 GPEPPEAQSPPPPPGCGCWKGHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
Db 241 GPEPPEAQSPPPPPGCGCWKGHGEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
QY 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQFTQRFSLSDRKVAKSL 360  
Db 301 ASPTSSGSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQFTQRFSLSDRKVAKSL 360  
QY 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTSTFWLLWANSVAVNPVLPCHHSFR 420  
Db 361 AVISIFGLCWAPYTLMLIIRAAACHGCVDPDYWTSTFWLLWANSVAVNPVLPCHHSFR 420  
QY 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445  
Db 421 RAFTKLLCPQKIKIOPHSSLEHCWK 445

## RESULT 4

US-08-985-090-2  
; Sequence 2, Application US/08985090  
; Patent No. 5882893  
; GENERAL INFORMATION:  
; APPLICANT: Andrew D.J. Goodearl  
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/985,090  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jean M. Silveri  
REGISTRATION NUMBER: 39,030  
REFERENCE/DOCKET NUMBER: MNI-032  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-985-090-2

Query Match 99.8%; Score 2357; DB 2; Length 445;  
Best Local Similarity 99.8%; Pred. No. 7.2e-161;  
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERAPPDGPNLNASGALAGDAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60  
DB 1 MERAPPDGPNLNASGALAGDAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60  
QY 61 ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120  
DB 61 ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120  
QY 121 SAFNIVLSYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
DB 121 SAFNIVLSYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240  
QY 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
DB 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
QY 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL 360  
DB 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL 360  
QY 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFR 420  
DB 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFR 420  
QY 421 RAFTKLLCPQKLIKIPHSLSLEHCWK 445  
DB 421 RAFTKLLCPQKLIKIPHSLSLEHCWK 445

## RESULT 5

US-09-165-543-2  
Sequence 2, Application US/09165543  
Patent No. 6093545

GENERAL INFORMATION:  
APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 28 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/165,543  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/042,780  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: MNI-032CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 227-7400  
TELEFAX: (617) 742-4214  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-165-543-2

Query Match 99.8%; Score 2357; DB 3; Length 445;  
Best Local Similarity 99.8%; Pred. No. 7.2e-161;  
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERAPPDGPNLNASGALAGDAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60  
DB 1 MERAPPDGPNLNASGALAGDAAAGARGFSAAWTAVLAALMALLIVATVGLNALVMLAFV 60  
QY 61 ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120  
DB 61 ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRWTFGRGLCKLWLVVDVLLCTS 120  
QY 121 SAFNIVLSYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
DB 121 SAFNIVLSYDRFLSVTRAVSYRAOQGDTRRAVRKMLLVWVLAFLLYGPAILLSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFYNWYFLITASTLEFPTPLSVTFNLSIYLNTOQRTRLRDLGAREAA 240  
QY 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
DB 241 GPEPPEAQSPPPPPGCGWCKQKGHEAMPLHRYGVGEAAVGAAGATLGGGGGGSV 300  
QY 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL 360  
DB 301 ASPTSSSSSGSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL 360  
QY 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFR 420  
DB 361 AVIVSIFGLCWAPYTLMIIRAACHGHCVPDYWYETSFWLLWANSVNPVLYPLCHHSFR 420  
QY 421 RAFTKLLCPQKLIKIPHSLSLEHCWK 445  
DB 421 RAFTKLLCPQKLIKIPHSLSLEHCWK 445

## RESULT 6

US-09-949-016-10930  
; Sequence 10930, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10930  
; LENGTH: 449  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-10930

Query Match 99.8%; Score 2357; DB 4; Length 449;  
Best Local Similarity 99.8%; Pred. No. 7.3e-161;

Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MERAPPDGLNASGALAGDAAAAGARGFSAATAVLAALMALLIVATVGLNALVMLAFV	60
DB	5	MERAPPDGLNASGALAGDAAAAGARGFSAATAVLAALMALLIVATVGLNALVMLAFV	64
QY	61	ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRTWFGRLGCKLWLVVDVLLCTS	120
DB	65	ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRTWFGRLGCKLWLVVDVLLCTS	124
QY	121	SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180
DB	125	SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	184
QY	181	SSIPGHCYAEFFYNNYFLITASTLEFPTPLSVTFNLSIYVNTQRTLRDLGAREAA	240
DB	185	SSIPGHCYAEFFYNNYFLITASTLEFPTPLSVTFNLSIYVNTQRTLRDLGAREAA	244
QY	241	GPEPPEAQSPPPPPGCGWKQKGEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	300
DB	245	GPEPPEAQSPPPPPGCGWKQKGEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	304
QY	301	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL	360
DB	305	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL	364
QY	361	AVISIFGLCWAPYTLMIIRAACHGCVDPYVYETSWFLLWANSVNPVLYPLCHHSFR	420
DB	365	AVISIFGLCWAPYTLMIIRAACHGCVDPYVYETSWFLLWANSVNPVLYPLCHHSFR	424
QY	421	RAFTKLLCPQKLIQPHSSLEHCWK	445
DB	425	RAFTKLLCPQKLIQPHSSLEHCWK	449

## RESULT 7

US-09-891-053-20  
; Sequence 20, Application US/09891053  
; Patent No. 6750322  
; GENERAL INFORMATION:  
; APPLICANT: Itadani, Hiraku  
; APPLICANT: Takimura, Tetsuo  
; APPLICANT: Nakamura, Takao  
; APPLICANT: Kobayashi, Masahiko

; APPLICANT: Tanaka, Ken-ichi  
; APPLICANT: Hidaka, Yusuke  
; APPLICANT: Ohta, Masataka  
; TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
; BINDING PROTEIN: COUPLED RECEPTOR PROTEINS  
; FILE REFERENCE: 06501-083001  
; CURRENT APPLICATION NUMBER: US/09/891,053  
; CURRENT FILING DATE: 2001-09-17  
; PRIOR APPLICATION NUMBER: PCT/JP99/07280  
; PRIOR FILING DATE: 1999-12-24  
; PRIOR APPLICATION NUMBER: PCT/JP98/05967  
; PRIOR FILING DATE: 1998-12-25  
; PRIOR APPLICATION NUMBER: JP 11/145661  
; PRIOR FILING DATE: 1999-05-25  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 453  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-891-053-20

Query Match 99.8%; Score 2357; DB 4; Length 453;  
Best Local Similarity 99.8%; Pred. No. 7.3e-161;  
Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY	1	MERAPPDGLNASGALAGDAAAAGARGFSAATAVLAALMALLIVATVGLNALVMLAFV	60
DB	1	MERAPPDGLNASGALAGDAAAAGARGFSAATAVLAALMALLIVATVGLNALVMLAFV	60
QY	61	ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRTWFGRLGCKLWLVVDVLLCTS	120
DB	61	ADSSLRTONNFFLLNLAIISDFLVGAFICPLVYVYVLTGRTWFGRLGCKLWLVVDVLLCTS	120
QY	121	SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180
DB	121	SAFNIVLISYDRFLSVTRAVSYRAQQGDTTRAVRKMLLVWVLAFLLYGPAILSWEYLSGG	180
QY	181	SSIPGHCYAEFFYNNYFLITASTLEFPTPLSVTFNLSIYVNTQRTLRDLGAREAA	240
DB	181	SSIPGHCYAEFFYNNYFLITASTLEFPTPLSVTFNLSIYVNTQRTLRDLGAREAA	240
QY	241	GPEPPEAQSPPPPPGCGWKQKGEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	300
DB	241	GPEPPEAQSPPPPPGCGWKQKGEAMPLHRYGVGEAAVGAAGEATLGGGGGGSV	300
QY	301	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL	360
DB	301	ASPTSSSSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSFQRLSRDRKVAKSL	360
QY	361	AVISIFGLCWAPYTLMIIRAACHGCVDPYVYETSWFLLWANSVNPVLYPLCHHSFR	420
DB	361	AVISIFGLCWAPYTLMIIRAACHGCVDPYVYETSWFLLWANSVNPVLYPLCHHSFR	420
QY	421	RAFTKLLCPQKLIQPHSSLEHCWK	445
DB	421	RAFTKLLCPQKLIQPHSSLEHCWK	445

## RESULT 8

US-09-165-543-5  
; Sequence 5, Application US/09165543  
; Patent No. 6093545  
; GENERAL INFORMATION:

; APPLICANT: Andrew D.J. Goodearl and Sandra Gluckman  
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: LAHIVE & COCKFIELD, LLP  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: Massachusetts  
; COUNTRY: USA

ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: US/09/165,543  
APPLICATION NUMBER: 09/042,780  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
FILING DATE: 09/042,780  
ATTORNEY/AGENT INFORMATION:  
NAME: Elizabeth A. Hanley  
REGISTRATION NUMBER: 33,505  
REFERENCE/DOCKET NUMBER: MNI-032CP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)742-4214  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 445 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-165-543-5

Query Match 93.7%; Score 2213; DB 3; Length 445;  
Best Local Similarity 93.5%; Pred. No. 1.4e-150;  
Matches 417; Conservative 9; Mismatches 18; Indels 2; Gaps 2;  
QY 1 MERAPPDGLNAGSAGALAGDAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60  
DB 1 MERAPPDGLNAGSAGTLAGENAAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60  
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRTWTEGRLCKLWLVVDYLLCTS 120  
DB 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRTWTEGRLCKLWLVVDYLLCAS 120  
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180  
DB 121 SVFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGARE-A 239  
QY 241 GPEPPEAQSPPPP-PPGCGWQKGHEAMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299  
DB 240 GPEPPEAQSPPPPAPPSCWCPKGHEAMPLHRYGVGEAGPGVEAGEAALGGSGGGA 299  
QY 300 VASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359  
DB 300 AASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359  
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWTYETSFLLWANSVNPVLYPLCHHSF 419  
DB 360 LAIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWTYETSFLLWANSVNPVLYPLCHYSF 419  
QY 420 RRAFTKLLCPQKLIKPHSSLSHCWK 445  
DB 420 RRAFTKLLCPQKLIKPHGSLQOCWK 445

RESULT 9  
US-09-891-053-25  
Sequence 25, Application US/09891053  
Patent No. 6750322  
GENERAL INFORMATION:  
APPLICANT: Itadani, Hiraku  
APPLICANT: Takimura, Tetsuo  
APPLICANT: Nakamura, Takao

APPLICANT: Kobayashi, Masahiko  
APPLICANT: Tanaka, Ken-ichi  
APPLICANT: Hidaka, Yusuke  
APPLICANT: Ohta, Masataka  
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)  
TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS  
FILE REFERENCE: 06501-083001  
CURRENT APPLICATION NUMBER: US/09/891,053  
CURRENT FILING DATE: 2001-09-17  
PRIOR APPLICATION NUMBER: PCT/JP99/07280  
PRIOR FILING DATE: 1999-12-24  
PRIOR APPLICATION NUMBER: PCT/JP98/05967  
PRIOR FILING DATE: 1998-12-25  
PRIOR APPLICATION NUMBER: JP 11/145661  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25  
LENGTH: 445  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-891-053-25

Query Match 93.7%; Score 2213; DB 4; Length 445;  
Best Local Similarity 93.5%; Pred. No. 1.4e-150;  
Matches 417; Conservative 9; Mismatches 18; Indels 2; Gaps 2;  
QY 1 MERAPPDGLNAGSAGALAGDAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60  
DB 1 MERAPPDGLNAGSAGTLAGENAAAGGARGFSAANTAVLAALMALLIVATVGLGNALVWLAFV 60  
QY 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRTWTEGRLCKLWLVVDYLLCTS 120  
DB 61 ADSSLRTQNNFLLNLAIISDFLVGAFICPLYVPYVLTGRTWTEGRLCKLWLVVDYLLCAS 120  
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180  
DB 121 SVFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180  
QY 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGAREAA 240  
DB 181 SSIPGHCYAEFFYNNWYFLITASTLEFFTPFLSVTFNLSIYLNQRTLRDLGARE-A 239  
QY 241 GPEPPEAQSPPPP-PPGCGWQKGHEAMPLHRYGVGEAAVGAEGEATLGGGGGGGS 299  
DB 240 GPEPPEAQSPPPPAPPSCWCPKGHEAMPLHRYGVGEAGPGVEAGEAALGGSGGGA 299  
QY 300 VASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359  
DB 300 AASPTSSSGSSSRGTERPRSLKRGSKPSASSASLEKRMKMWVSQSTQRPRLSRDRKVKAS 359  
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWTYETSFLLWANSVNPVLYPLCHHSF 419  
DB 360 LAIVSIFGLCWAPYTLMIIRAACHGCHVDPDYWTYETSFLLWANSVNPVLYPLCHYSF 419  
QY 420 RRAFTKLLCPQKLIKPHSSLSHCWK 445  
DB 420 RRAFTKLLCPQKLIKPHGSLQOCWK 445

RESULT 10  
US-09-891-053-1  
Sequence 1, Application US/09891053  
Patent No. 6750322  
GENERAL INFORMATION:  
APPLICANT: Itadani, Hiraku  
APPLICANT: Takimura, Tetsuo  
APPLICANT: Nakamura, Takao  
APPLICANT: Kobayashi, Masahiko  
APPLICANT: Tanaka, Ken-ichi  
APPLICANT: Hidaka, Yusuke  
APPLICANT: Ohta, Masataka  
TITLE OF INVENTION: NOVEL GUANOSINE TRIPHOSPHATE (GTP)

```
; TITLE OF INVENTION: BINDING PROTEIN-COUPLED RECEPTOR PROTEINS
; FILE REFERENCE: 06501-083001
; CURRENT APPLICATION NUMBER: US/09/891,053
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/JP99/07280
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: PCT/JP98/05967
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: JP 11/145661
; PRIOR FILING DATE: 1993-05-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-891-053-1

Query Match      87.1%; Score 2057; DB 4; Length 413;
Best Local Similarity 87.9%; Pred. No. 1.8e-139;
Matches 392; Conservative 8; Mismatches 12; Indels 34; Gaps 3;

QY 1 MERAPPDGLNAGSALAGDAAGGARGSAANTAVLAALMALLIVATVLGNALVMLAPV 60
Db 1 MERAPPDGLMNASGTLAGEAAGGARGSAANTAVLAALMALLIVATVLGNALVMLAPV 60
QY 61 ADSSLRTONNFFLLNALISDFLVGAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNFFLLNALISDFLVGAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCAS 120
QY 121 SAFNVLISYDFLSVTRAVSYRAQQDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180
Db 121 SVFNVLISYDFLSVTRAVSYRAQQDTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGG 180
QY 181 SSIPGHCVAEFPYNYFLITASTLEFFTPFLSVTFNLSIYLNQTRRLDGLDAREAA 240
Db 181 SSIPGHCVAEFPYNYFLITASTLEFFTPFLSVTFNLSIYLNQTRRLDGLDGRE-A 239
QY 241 GPEPPEAQPSPPP-PPGCGWCKQKCHGEMPLHRYGVEAAGAEATLGGGGGGGS 299
Db 240 GPEPPEAQPSPPPAPPSCWCKMPKGHEAMPLH----- 273
QY 300 VASPTSSSGSSRGTERPRSLKRGKPSASSASLEKRMKMWVSQSFQRFRLSRDRKVKAS 359
Db 274 -----SGSSSSRGTERPRSLKRGKPSASSASLEKRMKMWVSQSFQRFRLSRDRKVKAS 327
QY 360 LAVIVSIFGLCWAPYTLMIIRAACHGHCVPDYVYETSFLLWANSVNPVLYPLCHHSF 419
Db 328 LAIIVSIFGLCWAPYTLMIIRAACHGRCIPDYVYETSFLLWANSVNPVLYPLCHYSF 387
QY 420 RRAFTKLLCPQKLTQPHSSLEHCWK 445
Db 388 RRAFTKLLCPQKLVQPHGSLQCKWK 413

RESULT 11
US-08-985-090-5
; Sequence 5, Application US/08985090
; Patent No. 588593
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl
; TITLE OF INVENTION: MUSCARINIC RECEPTORS AND USES THEREFOR
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; TITLE OF INVENTION: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,090
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jean M. Silveri
; REGISTRATION NUMBER: 39,030
; REFERENCE/DOCKET NUMBER: MMI-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-985-090-5

Query Match      77.4%; Score 1828; DB 2; Length 362;
Best Local Similarity 92.8%; Pred. No. 3.8e-123;
Matches 337; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

QY 84 GAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYR 143
Db 1 GAFCLPLYVPYVLTGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSYR 60
QY 144 AQGGTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGGSSIPGHCVAEFPYNYFLITAS 203
Db 61 AQGGTRRAVRKMLVWVLAFLLYGPAILLSWEYLSGGSSIPGHCVAEFPYNYFLITAS 120
QY 204 TLEFFTFLSVTFNLSIYLNQTRRLDGLDAREAAAGPEPPEAQPSPPP-PPGCGWCK 262
Db 121 TLEFFTFLSVTFNLSIYLNQTRRLDGLDGRE-AGPEPPEAQPSPPPAPPSCWCK 179
QY 263 QKGHEAMPLHRYGVEAAGAEATLGGGGGGSVASPTSSSGSSRGTERPRSLKR 322
Db 180 PKGHGEMPLHRYGVEAGPGVEAGEAALGGGGGGGAAASPTSSSGSSRGTERPRSLKR 239
QY 323 GSKPSASSASLEKRMKMWVSQSFQRFRLSRDRKVKASLAVIVSIFGLCWAPYTLMIIRA 382
Db 240 GSKPSASSASLEKRMKMWVSQSFQRFRLSRDRKVKASLAVIVSIFGLCWAPYTLMIIRA 299
QY 383 ACHGHCVPDYVYETSFLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKLTQPHSSLEH 442
Db 300 ACHGRCIPDYVYETSFLLWANSVNPVLYPLCHYSFRRAFTKLLCPQKLVQPHGSLQ 359
QY 443 CWK 445
Db 360 CWK 362

RESULT 12
US-09-165-543-32
; Sequence 32, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
```

```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,543
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,780
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Elizabeth A. Hanley
; REGISTRATION NUMBER: 33,505
; REFERENCE/DOCKET NUMBER: MNI-032CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 362 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-165-543-32

Query Match      77.4%; Score 1828; DB 3; Length 362;
Best Local Similarity 92.8%; Pred. No. 3.8e-123;
Matches 337; Conservative 8; Mismatches 16; Indels 2; Gaps 2;

QY 84 GAFCLPLVYVYLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYR 143
Db 1 GAFCLPLVYVYLTGRWTFGRGLCKLWLVVDYLLCASSVFNVLISYDRFLSVTRAVSYR 60
QY 144 AQGGTRAVRKMVLVWVLAFLYPAILSWELSGGSIPEGHCVAEPFYNNWYFLITAS 203
Db 61 AQGGTRAVRKMVLVWVLAFLYPAILSWELSGGSIPEGHCVAEPFYNNWYFLISAS 120
QY 204 TLEFFTFLSVTFNLSIYNTQRTLRDLGDAREAAAGPEPPPEAQPSPPPP-PPGCGWGCW 262
Db 121 TLEFFTFLSVTFNLSIYNTQRTLRDLGDRE-AGPEPPPPDAQSPPPPPAPPCWGCW 179
QY 263 QHGHEAMPLHYRHYGVEAAVGAEGEATLGGGGGGGVSASPTSSSGSSSRGTERPRSLKR 322
Db 180 PKHGHEAMPLHYRHYGVEAGPGVEAGEAALGGGGGGGAAASPTSSSGSSSRGTERPRSLKR 239
QY 323 GSKPSASSASLEKRMKWSQSTQRFRLSRDRKVAKSLAVIUSIFGLCWAPYTLMIIRA 382
Db 240 GSKPSASSASLEKRMKWSQSTQRFRLSRDRKVAKSLAVIUSIFGLCWAPYTLMIIRA 299
QY 383 ACHGHCVDPYWTYSFLLWANSVNPVLYPLCHHSFRRAFTKLLCPQKLIKPHSSLEH 442
Db 300 ACHGRCPDYWTYSFLLWANSVNPVLYPLCHYSFRAFTKLLCPQKLIKVPHGSLEQ 359
QY 443 CWK 445
Db 360 CWK 362

RESULT 13
US-09-524-162-2
; Sequence 2, Application US/09524162
; Patent No. 6355452
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; TITLE OF INVENTION: HUMAN HISTAMINE H3 GENE VARIANT-2
; FILE REFERENCE: GP-70681
; CURRENT APPLICATION NUMBER: US/09/524,162
; CURRENT FILING DATE: 2000-03-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 351
; TYPE: PRT

; ORGANISM: HOMO SAPIENS
; US-09-524-162-2

Query Match      77.1%; Score 1820; DB 3; Length 351;
Best Local Similarity 78.7%; Pred. No. 1.4e-122;
Matches 350; Conservative 1; Mismatches 0; Indels 94; Gaps 2;

QY 1 MERAPPDGLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVIGNALVMAFV 60
Db 1 MERAPPDGLNASGALAGDAAAAGGARGFSAAWTAVLAALMALLIVATVIGNALVMAFV 60
QY 61 ADSSLRTONNPFLLNLAIISDELVGAFCLPLYVYVLTGRWTFGRGLCKLWLVVDYLLCTS 120
Db 61 ADSSLRTONNPFLLNLAIISDELV-----GRWTFGRGLCKLWLVVDYLLCTS 106
QY 121 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLVWVLAFLYGPAILSWELSGG 180
Db 107 SAFNVLISYDRFLSVTRAVSYRAOQGDTRRAVRKMLVWVLAFLYGPAILSWELSGG 166
QY 181 SSIPEGHCVAEPFYNNWYFLITASTLEFFTFLSVTFNLSIYNTQRTLRDLGDAREAA 240
Db 167 SSIPEGHCVAEPFYNNWYFLITASTLEFFTFLSVTFNLSIYNTQRTLRDLGDAREAA 226
QY 241 GPPEPPPEAQPSPPPPPGCGWCGKCHGEAMPLHRYGVGEAAVGAEGEATLGGGGGGSV 300
Db 227 GPPEPPPEAQPSPPPPPGCGWCGKCHGEAMPLH----- 259
QY 301 ASPTSSSGSSSRGTERPRSLKRSGKPSASSASLEKRMKWSQSTQRFRLSRDRKVAKSL 360
Db 260 -----RKVAKSL 266
QY 361 AVIVSIFGLCWAPYTLMIIRAACHGCHVDPYWTYSFLLWANSVNPVLYPLCHHSFR 420
Db 267 AVIVSIFGLCWAPYTLMIIRAACHGCHVDPYWTYSFLLWANSVNPVLYPLCHHSFR 326
QY 421 RAFTKLLCPQKLIKPHSSLEHCWK 445
Db 327 RAFTKLLCPQKLIKPHSSLEHCWK 351

RESULT 14
US-09-414-010-2
; Sequence 2, Application US/09414010
; Patent No. 6204017
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsema, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/414,010
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-414-010-2

Query Match      30.7%; Score 724; DB 3; Length 390;
Best Local Similarity 38.6%; Pred. No. 3.3e-44;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

QY 30 SAAWTAVLAALMALLIVATVIGNALVMAFVADSSLRTONNPFLLNLAIISDELVGAFCLP 89
Db 11 SLSTRVTLLAFVMSLVAFALMIGNALVILAFVVDKRLHRSSYFFLLNLAIISDFVGVISIP 70
QY 90 LYVPVYLTGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISYDRFLSVTRAVSYRAOQGD 149
```



```
Db 71 LYIPHTLP-EDWFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNVAVSYRQHTGV 129
QY 150 RRAVRKMLLVVLAFLLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFVNNYFLITASTL 205
Db 130 LKIVTLMAVAVVLAFLVNGPMLVSESWK-----DEGSECEPGFFSEWILAITSF 181
QY 206 EFFTFFLSVTFPNLSIYLNIOQRTRLRDGAREAGPPEPPPAQSPPPPCWGCWQKG 265
Db 182 EVVIPVILVAYFNMIY-----WSLWKRD 205
QY 266 HGEAMPLHRYGVGEAAVGAEEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
Db 206 HLSRCQSH-----PGLTAVSSNICGHSFGRLLSSRRSLASASTEVPAFHSERQRKS 257
QY 319 SLKRGSKPSASASLEKRMKMWVSQSFT-----QRFRLSRDRKVAKSLAVIVSIFGLCWA 372
Db 258 SLMFSSRTKMNSNTIASKMGFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
QY 373 PYTLLMIIRAACHGHCVP-DYHYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLLCPQK 431
Db 318 PYSLFTIIVLSFYSSATGPKSVMYRIAFWLQWNSFVNPLLYPLCHKRFQKAPLKIFC--- 374
QY 432 LKIQP 436
Db 375 IKQP 379
```

## RESULT 15

```
US-09-812-216-2
; Sequence 2, Application US/09812216
; Patent No. 6613533
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monama, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2
```

```
Query Match 30.7%; Score 724; DB 4; Length 390;
Best Local Similarity 38.6%; Pred. No. 3.3e-44;
Matches 164; Conservative 56; Mismatches 131; Indels 74; Gaps 10;

QY 30 SAAWTAVALAALMALIVATVLGNALVLAFAVDASLRTQNNPFLNLALISDFLVGAFQIP 89
Db 11 SLSTRVTLAFLMSLVAFALMUGNALVILAFVVDKRLHRSSYFFLNLAISDFVGVISIP 70
QY 90 LYVPVLTGRWTFGRGLCKLMLVVDYLLCTSAFNVLISYDRFLSVTRAVSYRAQQGDT 149
Db 71 LYIPHTLP-EDWFGKEICVFWLTTDYLLCTASVYNIIVLISYDRYLSVSNVAVSYRQHTGV 129
QY 150 RRAVRKMLLVVLAFLLYGPAIL---SWEYLSGGSSIPEG-HCYAEFFVNNYFLITASTL 205
Db 130 LKIVTLMAVAVVLAFLVNGPMLVSESWK-----DEGSECEPGFFSEWILAITSF 181
QY 206 EFFTFFLSVTFPNLSIYLNIOQRTRLRDGAREAGPPEPPPAQSPPPPCWGCWQKG 265
Db 182 EVVIPVILVAYFNMIY-----WSLWKRD 205
```

```
QY 266 HGEAMPLHRYGVGEAAVGAEEATLGGGGGGSVASPTSSSGSS-----SRGTERPR 318
Db 206 HLSRCQSH-----PGLTAVSSNICGHSFGRLLSSRRSLASASTEVPAFHSERQRKS 257
QY 319 SLKRGSKPSASASLEKRMKMWVSQSFT-----QRFRLSRDRKVAKSLAVIVSIFGLCWA 372
Db 258 SLMFSSRTKMNSNTIASKMGFSQSDSVALHQREHVELLRARRLAKSLAILLGVFAVCWA 317
QY 373 PYTLLMIIRAACHGHCVP-DYHYETSFWLLWANSVNPVLYPLCHHSFRRAFTKLLCPQK 431
Db 318 PYSLFTIIVLSFYSSATGPKSVMYRIAFWLQWNSFVNPLLYPLCHKRFQKAPLKIFC--- 374
QY 432 LKIQP 436
Db 375 IKQP 379
```

Search completed: June 2, 2005, 20:41:49  
Job time : 29 secs